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Vogel, Nancy

Sent:

Monday, June 12, 2006 9:13 AM

To: Subject: STIC-Biotech/ChemLib sequence search 09/896,888

please do a sequence search, including interference files, of

SEQ ID NO:1 (entire), bp. 351-527 of SEQ ID NO: 1,

of 09/896888, and return results to me on paper asap.

Thanks
Nancy Vogel
Patent Examiner
Art Unit 1636
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Mail Box: Remson 2C70
(571) 272-0780

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Searcher: ______ Searcher Phone: _____ Date Searcher Picked up: _____ Date completed: _____ Searcher Prep Time: _____ Online Time: _____ Online Time: _____ Searcher Prep Time: _____ Searcher Prep Time: _____ Online Time: _____ Searcher Prep Time: ______ Searcher Prep Time: _______ Searcher Prep Time: ________ Searcher Prep Time: ________ Searcher Prep Time: ________ Searcher Prep Time: ___

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Type of Search

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Inventor: Litigation:_____

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Lo-SEP-2001

PF 26-MAR-1998 JP 1998541010

PR 27-MAR-1997 US 60/049946, 28-JAN-1998 CA
THOMAS A GRIGLIATTI, DAVE A THEILMANN, THOMAS
A PFEIFER, DWAYNE D
PI HEGEBUS
PI HEGEBUS
PC CL2N15/85, C12N5/06, C12N15/77

CC Insect expression "FH Key
FT Source source 1 (bases 1 to 564)
3 Grigliatti, T.A., Theilmann, D.A., Pfeifer, T.A. an Insect expression vectors
3 Patent: JP 2001516225-A 1 25-SEP-2001;
THE UNIVERSITY OF BRITISH COLUMBIA
OS Multicapsid nucleopolyhedrovirus
PN JP 2001516225-A/1
PD 25-SEP-2001
PF 26-MAR-1998 JP 1998541010
PF 26-MAR-1998 JP 1998541010
PR 27-MAR-1997 US 60/049946, 28-JAN-1998 CA 1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG BD070856 BD070856.1 GI:22616459 JP 2001516225-A/1. unclassified sequences.
1 (bases 1 to 564) BD070856 5 Insect expression vectors. unidentified unidentified 100.0%; ilarity 100.0%; Conservative 0; /organism='Multicapsid nucleopolyhedrovirus'. /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644" 0 Score 564; DB 2; Pred. No. 2.1e-185; Mismatches 0; 564 ď DNA Length 564; Indels linear Ç and Hegedus, D.D. PAT 27-AUG-2002 <u>.</u> Gaps P 60 0

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Theilmann,D.A. and Stewart,S.
Tandemly repeated sequence at the 3' end of the IB-2 baculovirus Orgyla pseudotsugata multicapsid nuclear virus is an enhancer element Virology 187 (1), 97-106 (1992)
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                                                                                                                                                                                                                                                                                                                                               transcriptional transactivator.
Orgyia pseudotsugata single capsid nuclopolyhedrovirus
Orgyia pseudotsugata single capsid nuclopolyhedrovirus
Viruses, dsDNA viruses, no RNA stage; Baculoviridae;
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                                                                                                        Original source text: Orgyia virus DNA.
                                                                                                                                                                                                                                                         Nucleopolyhedrovirus.

1 (bases 1 to 4170)
Theilmann,D.A. and Stewart,S.
Theilmann D.A. and Stewart,S.
Molecular analysis of the trans-activating IE-2 gene pseudotsugata multicapsid nuclear polyhedrosis virus Virology 187 (1), 84-96 (1992)
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/organism="Orgyia pseudotsugata nuclopolyhedrovirus" /mol_type="genomic DNA" /db xref="taxon:10450" 627. .3959
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GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
                                                                 GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                     GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                                                                 TTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCCACCACCACCTTTTTT
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/gene="IE-2"
2984. 3907
/gene="IE-2"
/note="ORF; homologous t
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/gene="IE-2"
2017. .2759
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2915. .2922
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2944. .>3907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAA46750.1"
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AQKEARDLQESWERQKQAHNVARNSSCEQVTALQTTLADMQAQLDRSEALSSTLAEHN
RAANVQIDSLRRAVQRLEAAQSAPVSUNVEFNDNARQNTNLHERFRSYVYSTVSDMMI
EDSIKSLQSHVFGAACLPCSVNVEINFPFDE"
3954. .3959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tranelation="msrsnnanaptpsnrrnlslvrgrrltysppdaasaqrasppr sapraaprrvilavgdeqaflasyalprgvrlhgdahfnppeddollfvdfaaga rqravnlheavrrherlrrelgemtrsptllyspsysptsprssptllmpeddqp arqqrlappndsdddrllrdedmtrsptlgpsprsprsprsprsptdlqp arqqllappndsdddrlllqumlssbabapollpappqpsyvlchicscyftdig nynsnfytstecnhavcfkcyvsivfgkesykcsicnrttiscraynrdgyvelstmstyrdsqafaalaelraatarahhdvnmarsdsq tyrdsqafaalkaatarahhdvnmarsdsq
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627. .634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               llrqqldvkeaelahesnarlklqkqnetlsannlslqhqlntqviesrvkmeqfkrq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/db_xref="GI:332541"
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                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 564; DB 10;
Pred. No. 2.4e-185;
Mismatches 0;
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                    SgS
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence update by submitter
On Oct 26, 2000 this sequence version replaced gi:2934903.
Location Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-OCT-1996) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA 3 (Dases 1 to 131995) Rohrmann, G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orgyia pseudotsugata MNPV Orgyia pseudotsugata MNPV Viruses; dsnviruses, no Niruses, no Niruses; dsnviruses, no Niruses; dsnviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-OCT-2000) Oregon State University, Chemistry, Corvallis, OR 97331-7301, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence update by submitter 4 (bases 1 to 131995) Rohrmann, G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-MAR-1998) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA
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Virology 229 (2), 381-399
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Rohrmann, G.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCTGTTACAGCGACACAACATG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 131995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
                                                  complement (123. .947)

/note="ORF1; pk-1; similar to AcMNPV ORF10"

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GALDNALVNIVRQLCDALNDLHNATGYIHNDVKLENVLYFGARDRVYLCDYGLCKRE
HSPVHHGTLEFFSPEKIRRHNYARSFDWYAVGVLAYKLLTGGRHPFERSADEVLDLAS
                    MRRRQQYNDPAALKNVRNLMARDFVFCLTRFNFECRSTDYKQIAKHSFLASRHDYI"
946. .2370
                                                                                                                                                                                                                                                            Number L22858"
                                                                                                                                                                                                                                                                           /note="similar to Autographa polyhedrosis virus (AcMNPV) o
note="ORF2; similar to AcMNPV ORF9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:11024985
                                                                                                                                                                                                                                                                                                                   mol_type="genomic DNA"
db_xref="taxon:262177"
                                                                                                                                                                                                                                                                                                                                                          organism="Orgyia pseudotsugata MNPV"
                                                                                                                                                                                                                                                                                                                                                                                   . .131995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131995 bp DNA circular VRL 25-MAR-: multicapsid nucleopolyhedrovirus, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no RNA stage; Baculoviridae;
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                                                                                                                                                                                                                                                                           deposited in GenBank
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gevthllikaqdyxbsncakwkkvtklcpqasmckglnpicnf"
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Rrfgflsrnvlvsacmavnvqvyapdatidmrhqptiyfrvcqnchamadvpapddhs
Iaryllabcgavlvldhpldyfgefbegvneulevqrinaggdl"
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HLNKGADKARKKKCABKAALKRVEIAADRHWLEAAAAPACADDGRWSTLSRAQLDDI
ARKKEIVDRHRLQLKQDSLLKQDRLKKR"
complement (4125. . 4739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAC59003.1"
/db_xref="GI:1911250"
/translation="MRKUNQASQYPEHLTTVHKRHRLQLSCVWCDDQRSWDPHSAKGL
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KHLDPLDHYMVAEDPFLGPGKNOKLTLFKEIRNVKPDTMKLIWMSGKEFLRETMTRF
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VGMNNEYRISLAKKGGCPINNIHASYTNSFESFVNRVIWENFYKPIVYIGTDSSEEE
EILIEVSLVPKVKEFAPDALLFTGPAY"
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RAVRLINRQAVLDLIKLAEDIYADTAYMQADQPEASSBHFATLIRMRLILIGYQDPDAR
RNINSVLARIEALLRYDVVNDAEVNVLSGDEYEEYSKYISYQQTFAQTFATASASQQTQ
TSLPRPQTGLSLERQTQASLPQQTPFDQDEMVSPPSFYHTTPAILPQTTQPPARTOTFSRP
SDEFVYVPGKERAVPDTRFKPPVPPKPEHLKSRPSSVATNAAGATPVAPPPPPFPSAD
VTTSMPPPPPFPSADVTTSMPPPPMFHLKSRPSSVATNAAGATPVAPPPPPPPPSAD
INNLLIDAWYAETNKKAGDUNRSALDQIKQGKTLKKTQPPADDGAPATDPRSTLLSEIRQ
GKTLKKLRKIEDQSSTQTLLKUVDTTDKTKTILKNFVTNIDRISKQEGEKDRLDTIT
KRPAVEHTDGNSTNNSDDMRDD"
                                                                                              complement (5669. .6151)
/note="ORF9; ptp-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                           CNRFLEAGDRAPAVIVKAAANGGQHSSLICDKV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4742. .4975)
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product="protein tyrosine phosphatase/protein_id="AAC59008.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC59004.1"
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                                                                                                                                                                                                                                                                                                                                                                                 note="ORF8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="ORF6; lef-2; similar to AcMNPV ORF6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="ORF5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="polyhedrin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (2533. .3270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="ORF4"
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                                                                                                                                                                                                                                                                                                                                                                                 similar to AcMNPV ORF4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to Acmnpv ORF5"
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MAPCKYTPERVQMMWDAIAYNDSRRLAFMTDRPRWYHAHNFFDS AAQLERYIVKNSISDVHYKELEEGGREWVIDADFKDCADKAELMLKVNVGATAFMLFF EGKEDAVQRIMFSGNRGFHLMLKFCGKFMDAPKSLREHWFNVFKQPAKLVSGDIRPG SFADCVRRAVHMYIGDAREDLYLRYWPDVDRDVFCNANKQIRAFFSYNYKGGDYSRCLTOQLQQRIKACSAGCLAGGTPFTSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MFSWMFGWWNAADEQVNAEFDEQAYRRYAVDQRAHSDLVRRDVF
RCHPFVFKFRYVLDETAGRCCSVVDFCKGLKISHDLLQRCNFPDRQHVRQLNELVLGAP
PAQPDSLGSLFATKHGLVQLLQOFSFANKNEFULAVGANKDHDRDNLLDKIBAYLNHV
KTLNTNSDKFISAHKSFKLEVGARFEQFEQRLQTLDTKLNALQCAAPTRTAPGVVFPR
DVTKHPHLAVFMGRVEDRGVTQLAFARGQEEHFRKRKLEFEEGNDVDVKGRAPNPLLA
VHCIKEBFANGGHKIRKLPKKVIEDVDCAVNVAKDIVKKAILNKT"
complement (9094. 9825)
                                                                                                                                                                                                                                                  /translation="MVFLIIALTLLATGARAASILAVLPTPAYSHHVVYRAYVHALVK
NCHAVTVIKPQLLDYAVQDEGGRVEQIDADMSAQQXKLVASSGVFRKRGVVADETTV
TADNYMGLIEMFKDQFDNANVRFELSTNRTFDAAVVVEAFADYALVFGHLFRPAFVIQI
APGYGLAENFERRRAVARHPLHYFTFGAAALTRRGGALSEWRLLNEFELLARRSDELL
KQQFGKSTFTIRQLADNYQLLLLNLHFVYDNNRPVFPSVQYLGGGLHLAQALPQRLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSLSSKLLVYAYYGSYNLPHDRYGESYHLYRIVHEHLTNTYYSN ASCVRRDIATARCLNSGHLCFDVARQLLDVSEVAARLSAWFRCSDATGLCADMQRALA DIRWHAPLAARRUGRANIFALDAIADIFSDVTNULQGIIGREMHFPRCSGLARVADVE DDIRADGWAYKKFCVLTYMHLVACGAVPAGSATRLRDAVAKHIGPNDEGNCAPAIAA VYGRFCAIGREHFAHKKTACMHILPQEMRNDLTPADERHPCFGVIKDFGRQCKDTYTD
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                                                                                                                                                                                   PLERRLNESVDGAVYVSFGSGIDTNSIHAEFLQMLLDTFANLNNYTVLWKVDDAVAAS
VALPRNVLAQKWFSQTAVLRHKNVVAFVTQAGLQSSDEALQARVPMVCLPMMGDQFHH
ARKLQQFGVARALDTAAVSAPQLQLAIREVIADGEAYRARIDKLRAVVEHDAAPDEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="late expression factor 1"
/protein_id="AAC59012.1"
/db_xref="GI:1911259"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="unknown"
/protein_id="AAC59011.1"
/db_xref="GI:1911258"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRTHADALYIHGTTDRQKNALFDLLCCVNASDIDADCYDCVVNKFYATQNKKYKM"
complement (8180...9142)
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hwthglnrsgylvcrymverlgvsptdaiarfetarghkiertnylqdllarkhvrgq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="mltsrrwaviytrtserncggawctngvrrrrqvhlpsvraram
fpdrwheytacgaviegtrllcfkvplnaelfeyvtsdedrwtaasvlarhsalgavi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (6129. .6791)
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pirhalglfvgdhihvyceaaptcaalpnampalydymvrrigegkrvlvhcyagasr
                                      /product="unknown"
/protein_id="AAC59014.1"
                                                                                                                                                                VKFTERVIKFNNDVNWPARSLKTTAANMAYSDYFVRFPL
                                                                                                                                                                                                                                                                                                                                                                     /product="ecdysteroid UDP-glucosyltransferase"
/protein_id="AAC59013.1"
/db_xref="GI:1911260"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ORF14; egt; similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="ORF13; lef-1; similar to AcMNPV ORF14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAC59010.1"
/db_xref="GI:1911257"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="ORF11;
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/product="protein tyrosine phosphatase 1"
/protein id="AAC5909.1"
/db_xref="GI:1911256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORF10;
                                                                                            codon_start=
                                                                                                               note="ORF15; similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
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100.0%;
Score 564;
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                                                                                                                  Acmnpv
DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AcMNPV ORF15"
                                                                                                                  ORF16"
Length 131995;
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AUTHORS
TITLE
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S64501/c
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                                                                                                                                                                                                                                                                                                                                             Orgyia pseudotsugata MNPV
Orgyia pseudotsugata MNPV
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.9=8.9 kda basic protein [Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus OpMNPV, Genomic, 1429 nt].
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                                                                                                                                                                                                                                    Wu,X., Stewart,S. and Theilmann,D.A. Characterization of an early gene coding for a highly basic 8.9K protein from the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                    S64501 .1 GI:404518
                                                                                                                                                        GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 136152] from the original journal article.
                                                                                                                                                                                                 8345350
                                                                                                                                                                                                                                                                                                                                   Nucleopolyhedrovirus.
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                                                                                                                                                                                                                  Gen. Virol. 74 (PT 8), 1591-1598 (1993)
                                                                                                                                                                                                                                                                                                                   (bases 1 to 1429)
                                       /db_xref="taxon:262177"
763. .990
                                                                        /organism="Orgyia pseudotsugata MNPV"
/mol_type="genomic DNA"
                                                                                                                                   Location/Qualifiers
/gene="p8.9"
/note="8.9 k
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JP 2005518194-A/17.
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563; Conservative
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 other sequences; artificial sequences.

1 (bases 1 to 2773)
Mouritsen,S., Voldborg,B., Bratt,T., Nielsen,F.S.
NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
Patent: JP 2005518194-A 17 23-JUN-2005;
Pharmexa A/S
OS Artificial sequence
PM JP 2005518194-A/17
PD 23-JUN-2005
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NOVEL IMMUNOGENIC MIMETICS
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//note="8.9 kda basic protein"
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/codon start=1
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/db_xref="GI:404519"
/translation="MNSQKIRMAKQQQVRVARQHRAAKLGRLYKAKKLRAELCEKLQ
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Pred. No. 8.2e-185;
0; Mismatches 1;
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                                            GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
                                                                                           GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
                                                                                                                                           15-NOV-2002 JP 2003544079
16-NOV-2001 DK PA200101702,16-NOV-2001 US
n mouritsen,bjoern voldborg,tomas bratt,finn
                                                                                                                                                                                                                                                                                                                                                                                97.2%; Score 548; DB 2; L
llarity 100.0%; Pred. No. 9.4e-180;
Conservative 0; Mismatches 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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(2128) . . (213)
/note='PatI site'
mb (2204) . (2209)
/note='NcoI site'
mb (2284) . (2289)
/note='AvaI site'
mb /2294) . (2299)
mb /note='AvaI, SmaI, a
(2551) . (2556)
/note='ApaLI site'.
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(629)...(634
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(593). .(598)
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(586)..(591)
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(573). .(578)
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    CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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/note="ApaLI site"
2128. .2133
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593. .598
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2551. .2556
/note="ApaLI site"
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2294. .2299
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2284. .2289
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2204. .2209
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/db_xref="taxon:32630"
/note="p2ZOp2F expression
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB175497 2005 AB175497 DNA linear VRL 29-MAR-2005 Hyphantria cunea nucleopolyhedrovirus ie2, hycu-ep32, odv-e56 gene for immediate early gene 2, early protein 32, occlusion derived virus envelope protein 56, partial and complete cds.

AB175497 COCCUPATION OF THE PROPERTY OF THE PROPERT
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Shirata, N., Ikeda, M. and Kobayashi, M.
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Ikeda,M., Shikata,M., Shirata,N., Chaeychomsri,S. and Kobayashi,M. Gene organization and sequencing of the Hyphantria cunea
                                                                                   Ikeda, M., Yanagimoto, K. and Kobayashi, M. Identification and functional analysis o nucleopolyhedrovirus imp genes Virology 321 (2), 359-371 (2004)
                                                                                                                                                                                                                                                                                                                Hyphantria cunea nucleopolyhedrovirus Hyphantria cunea nucleopolyhedrovirus Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                            Identification and characterization of Hyphantria cunea nucleopolyhedrovirus homologous repeated regions
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RNLGngryepgyllsnnQfisagdinritrsndvprirnvfQgindpQinslnQlrra
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1877. .>2284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="hycu-ep32"
                                                                                                                                                                                          25, 281-290
                                                                                                                                                                                                                                                                                                                                                                                                        GI:86198125
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                                                                                                                                                                                                                                                   Ikeda, M. and Kobayashi, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 138.4; DB 10;
Pred. No. 2.5e-36;
0; Mismatches 46;
                                                                                                                                                                                            (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic
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ic DNA, complete genome.
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-AUG-2005) Motoko Ikeda, Nagoya University, G: School of Bioagricultural Sciences; Chikusa, Nagoya, Aichi 464-8601, Japan (E-mail:mochiko@agr.nagoya-u.ac.jp, Tel:81-52-789-4036) Fax:81-52-789-4036)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleopolyhedrovirus genome Unpublished (bases 1 to 132959)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ikeda, M. and Kobayashi, M.
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VEMNNEYRISLAKRGGGCPIMNIHSEYTNSFEQFVNRVIWSNFYKPIVYIGTDSGEEE
                                                                                                       complement (3168. .3413)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVNAPFDAKVSELSTYANQLSANQLLASSVA"
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complement(735. .2354)
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/note="orf3 pk1"
                                                                                                                                                                                                                                                                                                                                                                                                                                             2353. .3
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                                                                                                                                                                                                                                                                                                                                                          /gene="pkl"
                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="pk1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="HynVgp002"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="1629capsid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Hyphantria cunea nucleopolyhedrovirus"
| mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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353. .3177
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. .738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAB72295.1"
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QTPQPAFEPQEDVETCHICSCTFTDIKNYNSRYTSSSCHAPCFKCYVSIVENKEA
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DNNSCNLSIFKIDNLFKQKEYNGFNDRRRRTACALNNQNIDVLKYKEDFDDDDTQTNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNAVVSCKFIKKTGDRVPFCQQFVBAVQFIKQRCAADADDDEPAVSQNNKLIQQETER
LQKTVDKHKQEAERLQEIVDKHKQEAERLQETVNKYKQBEERLQEIINCQKCQHDIAW
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NDENDEHHGHYQLEIKKNVAVNVEFNENARQKTNLHEQFRSRVYSTVADMMIEDKIKS
                                                        VALKQIRQIIMSQLYQRVEINVNNAMATENFDMLIN"
                                                                                           SLKMLSVTSTGNFNILFPETNNASWKKLASNNLITVYDNQQETPVIQTFNKSVEPFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (5764. .6891)
/gene="ie2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name="hrl" complement(5764. .6891)
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                                                                                                                                                                                                                                                                                                                                                              /locus_tag="HynVgp008"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             7456.
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7249. .7434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ep32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus_tag="HynVgp007"
/note="orf7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="HynVgp006"
/note="orf6 ie2"
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456. .8394
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Hyink, O., Dellow, R.A., and Ward, V.K.
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                                                                                                                       nucleopolyhedrovirus
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                                                  (bases 1 to 118584)
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                                                                                                                                                                                Ward, V.K.
                                                                                                                                                 complete sequence of the
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//tb_xre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   postvittana nucleopolyhedrovirus, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MPKNMAALHRSMETGPPTPSHTLFNTATELPDNLNLLEGTYEAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="HynVgp010" complement(9807. .11489)
                                                                                                                                                                                                             Dellow, R.A., Olsen, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (9807. .11489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="HynVgp009"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="HynVgp009"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="odv-e56"
                                                                                                                                                                                                                                                                                                                                                                                                                             GI:15213125
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                                                                                                                    genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 138.4;
Pred. No. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118584 bp
                            Olsen, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                     RNA stage; Baculoviridae;
                                                                                                                                                 Epiphyas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3e-36;
                            Caradoc-Davies, K.M.B.,
                                                                                                                                                                                                             Caradoc-Davies, K.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                 postvittana
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                               Drake, K.
                                                                                                                                                                                                                Drake, K.
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunedin,
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VGMNNEYRISLAKKGGGCPIMNIHSEYTNSFESFVNRVIWENFYKPIVYIGTDSGEEE
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RTNSELPKLLDNVFSLLDRKPRSVENVNEAKNILDNLKERVKLTSNQLDNAEAQSLYI
NDPNQFYIQVEDLIFAGRYADAKWHLDLAITESGNDERLRRLKKFANDLDAVVV"
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tyrlmtavlolkilarniyndtaymitotynnikfdanafutiliagpeahnvkonligg
tyrlmtavlolkilarniyndtaymitotynnikftyttomkrylt
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psudlipepppppllsgomypppppiegmothinatiagnikgekvutdargomli
psudlipeppppppllsgomypppppiskon
                                                                                   complement (2717.
                                                                                                                                                                                                                                                                                                                                                                                     complement (2104. .2715)
                                                                                                                                                                                                                                                                                                                                                                                                                  complement (2104. .2715)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="ORF1"
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/note="EppoMNPV"
join(117505. .118584,1
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                                                                                                                                                                                                                                                                                                                                    note="ORF4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="ORF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="Pol"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                      .3070)
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NRSVPKCHPETFKFRYVIDDDNGRCCRVVDFCKGLEINHELMINCKWDSKHVRHINEI VFKTPPVEISPDSMGTVYATKIGLIQILSFEYKDDVILAIKTDKGYDCDDVEDNI KTVLKHIKTLNVNSDKEINAHKLFENQVCARFEQLEQRLETLERVPDAPTMPGVIFPR DVNKHQHLAVFVNQERGNTQIGFARGQEEYFRKKLEFEEEDMHKMLETVHPNPQMAV QCIKDRFISNGYKIKKVSNRRRVIEVDCNINAAKDIVNNVIIS"
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KKSDTVGMWYNKFCYLTYMYKIINKSVPAELLTRLQKAVVEXIQPNAGDKYNCAEVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVYGRFCGIGKQHFAEHKTANMHIMFKSMRGQTTMVDERYKSFSVIKDFSRHCKETYL
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complement (5163..5516)
ahcmoravnmyodollosskpdelilhfwpdvdkdvfcnptkoirapfsynhkgtofs
                                                                                                                                                                                                                                                                                                                             complement (6427.
                                                                                                                                                                                                                                                                                                                                                               /gene="lef-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3426...3935)
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complement (3426...3935)
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Matches
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Rachiplusia ou multiple nucleopolyhedrovirus,
AY145471
2 (bases 1 to 131526)
Harrison, R.L. and Bonning, B.C.
                                                           Harrison, R.L. and Bonning, B.C.
The nucleopolyhedroviruses of Rachiplusia ou and falcifera are isolates of the same virus
J. Gen. Virol. 80 (Pt 10), 2793-2798 (1999)
                                                                                                                                                                          Viruses; dsDNA viruses,
Nucleopolyhedrovirus.
                                                                                                                                                                                                                            Rachiplusia ou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACGAATCGTAGACTATTTAACTTGAATAGTCTACACTGTTCTATACGCTCCTAATACA 114673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCTTTTTGCACTGCAAAAAAGTTCATTTTTTTCTGAGACCCTATACACAGTACAAAAA 114733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACTACACATTGAATTTTTTTTGTÄGTGCAAAAATTACATAT 114630
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7254. .8732
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DKAIKFTERVIKFGHDITYPARSLKSPAANLDQSNYFISFPL"
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LGSDVITSAANKRFKILNVEKVVNAKFIVQQTLHNGFNNYPNTH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MHFAVLLTLLAAQAHAANILAVLPTPAYSHHLVYKAYVQALANK
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IAPGYGLDENFDTAGAVARHPKYYPNIWRSTFVGGTAGALSEWRLYNEFELLARYSDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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Pred. No. 6.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-AUG-2002) Entomology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonning, B.C.
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                                                                                                                                                                             /translation="MAVIFNNKQLLADDSIENGGELFLLNGSYSILENYVNPVLLKNG
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TMRSGTIHPIKKDIYIYDNKKFTLYDRYIYGYDNYVNFYEEKNEKEKEEEDDRQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="mkltykmasllkyalrltreykeniiphfdhltrlrdlidgmik
Nedvqrfnrtsrndlisacmqinvhtympnatidmrkqpnciyfricqychleadvps
Pdnhsvyrylcvacgtplvidhfldvfghteegvnellevqrinaggdl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mppsrwhnylqcgqvikdsnlicfktplrpelfayvtseedvwt
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                                                                                                                                                                                                                                            /product="unknown"
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complement(2429. 3064)
                                                                                                                                                                                                                                                                                                                                                                                              /translation="mANALYNVWSPLISASCLDKKATYLIDPDDFIDKLTLTPYTVFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (962.
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/db_xref="GI:23476562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="consists of 30 bp imperfect palindromes; hrl; replication origin"
                                                                  /product="polyhedrin"
                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                     /note="orf603; ro5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="lef-2; ro4; ac6-like"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ro3; ac5-like"
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join(131515. .131526,1.
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    translation="MPDYSYRPTIGRTYVYDNKYYKNLGSVIKNAKRKKHLIEHEEEE
                                                                                                             note="polh;
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                                                                                                               ac8-like"
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PNPNNNVVGWMYNKFCVVTTVHRINGSVPABLLAPRLSGREFYFTRERSSFDYDRIHL
DESYNCTRVIABIYGRFGG1GKEHFSKHKLSCHHILFQYLRGKTTQEERSFPCYRVIF
DESYNCTRVIABIYGRFGG1GKEHFSKHKLSCHHILFQYLRGKTTQEESFPCYRVIFEAFL
DEGRQCKDVYKNLKDVFDVLHAHSMSDKDKNSLMDLLCVMDCEEIDVDCFYYIFEAFL
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| SKRANKPDVKTVQSLENVFTSSQLYTNDNDEKNTKAHDILNVEALLQNKTQTNIDKA
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/note="rol1; ac13-like"
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                                                                                                                                              complement (9128. .9931)
                                                                                                                                                                                VVTESQNGTVTFPRDITKHQHLAVFSERIDDRIKLAFVLGQERHFRKRKMRFEDDMEV
LYDGVHPNPLLAIQCINEKLYDKHYKIRKIAKRVIDVNCTPNVVKEVIQEVL"
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IPALTYHPKDYKFNELLKYVQQLSVNQQRTESSA"
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DEFINITION
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Best Local Sim
Matches 124;
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                                                                                                                                                 major early protein PE-38.
Autographa californica nucleopolyhedrovirus
Autographa californica nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                               Autographa californica nuclear polyhedrosis virus major early protein (PB-38) gene, complete cds.
1987375
Original source text: Autographa californica nuclear polyhedrosis
                                                                       1 (bases 1 to 1511)
Krappa, R. and Knebel-Morsdorf, D.
Identification of the very early
                                                                                                                                                                                                                                                                                              M62488.1 GI:332470
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                                                 65 (2), 805-812 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MLFTIIYLVFLRGALCGCALSAFINAHQPKQVIIVPGRSKAKHQ/
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Pred. No. 2.2e-23;
0; Mismatches 37
                                                                             transcribed baculovirus gene PE-38
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Best Local Similarity
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                                                          unclassified sequences.

1 (bases I to 133894)

Bishop, D. Possee, R. and Ayres, M.
AUTOGRAPHA CALIFORNICA COMPLETE GENOME
PATENT: WO 9601320-A I 18-JAN-1996;
NATURAL ENVIRONMENT RES (GB)
Other publication AU 2897295 960125.
Location Qualifiers
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Sequence 1 from Patent W09601320.
A48542
A48542.1 GI:2302312
                                                                                                                                                                                                                         unidentified
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1433. .1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLI PTTCDHGFCFKCVINLQSNAMNI PHSTVCCPLCNTQVKMMRSLKPNAVVTCKFYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="PE-38"
379. .1453
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352. .357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLVYSTISELFIENRVHSIQNYVYAGTSAASSCDVNVTVNFGFEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="immediate-early
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Autographa c
/mol_type="genomic DNA"
/db_xref="taxon:46015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="PE-38"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.0%;
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Pred. No. 2.2e-23;
0; Mismatches 41;
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L22858/c
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                                                                   gene
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Ayres,M.D., Howard,S.C., Kuzio,J., Lopez-Ferber,M. and Possee,R.D.
The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Autographa californica nucleopolyhedrovirus
Autographa californica nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Bacul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuzio, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 202 (2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyhedrosis virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
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                                                                                                 /codon_start=1
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/db_xref="GI:559070"
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VKEFTEKCPGMLVGVHCTHGINRTGYMVCRYLMHTLGIAPQEAIDRFEKARGHKIERQ
                                                                                                                                                                                                                                                                                                                                                         /note="5 Copies of 30 bp imperfect palindromic sequence;
the EcoRI site in the first palindrome is at residue 1 of
the linearized genome"
                 /note="synonym: AcOrf-2"
complement(1041. .2027)
                                                                                                                                                                                                                                                                                                         /rpt_type=dispersed
                                                                   complement (1041.
                                                                                                                                                                                                                                                                                                                                                                                                                              join(133883. .133894,1. .445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Autographa californica
/mol_type="genomic DNA"
                                                   /gene="Ac-bro"
                                                                                                                                                                                                                                      /gene="Ac-ptp"
                                                                                                                                                                                                                                                                       /note="synonym:
                                                                                                                                                                                                                                                                                         /gene="Ac-ptp"
                                                                                                                                                                                                                                                                                                                                          function="enhancer; replication
                                                                                                                                                                                                                                                                                                                                                                                                            standard_name="hrl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:46015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (08-MAR-1999) NCBI, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:510708
                                                                                                                                                                                                                       note="PTP; 19288 Da primary translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          californica
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75.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133894 bp
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                                                                   .2027)
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                                                                                                                                                                                                                                                                                                                                         origin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20894, USA
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                                                                                                                                                                /note="synonym: AcOrf-7" complement(3759. .4364) /gene="Ac-ORF603"
                                                                                                                                                                                                                                                                                                                                                                     /note="LEF2; 23926 Da primary translation 
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SEDVQRFNRTNRNDLISACMQINVRTYMPNATIDMRKQPNCIYFRICQYCHLEADVPS
DDDHSVYRYLCVACGTPLVIDHPLDVFGHTEEGVNELLEVQRVNAGGEL"
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VAQKTEELVKKQEFIERIVAIKDKQIEAKDLQVTRVMTDLNRMYTGFQETMQKKDEIM
QKKDAQVTDLVAKVVDLSDRAVQYPADKRKHPVLCVTRDGTTFTAITGQKTYVENQKH
                                                                                                                                                                                                                     /gene="Ac-ORF603"
                                                                                                                                                                                                                                                           complement (3759.
                                                                                                                                                                                                                                                                                 HDSKCVGEVMHLLIKSQDVYKPPNCQKMKTVDKLCPFAGNCKGLNPICNY'
                                                                                                                                                                                                                                                                                                    /translation="manasynvwsplirascldkkatylidpddfidkltltpytvfy
NGGVLVKISGLRLYMLLTAPPTINEIKNSNFKKRSKRNICMKECVEGKKNVVDMLNNK
INMPPCIKKILNDLKENNVPRGGMYRKRFILNCYIANVVSCAKCENRCLIKALTHFYN
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sfdCnKflrsddmfpvvttitpkrtadyKitbyvgdvKtikpsnrplvesgplvreaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="AcOrf-4"
complement(2295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MQIKTVLLAFAMFAALNAQHVLAACAETGAVCVHNDECCSGACS
PIFNYCLPQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="12435 Da primary translation product"
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/protein id="AAA6635.1"
/db_xref="GI:559074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="AcOrf-5"
2779. .3108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="conotoxin-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2084. .2245)
/gene="Ac-ctx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (2084. . 2245)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="marvkigefkfgedtfnlryvlerdqqvrfvakdvanslkytvc
bkairvhvdnkykslfeqtiqnggftsnsvvkrgdplylqphtvlitksgviqlinks
                                                                                                                                             note="ORF603 peptide; 23612"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Ac-lef2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="synonym: AcOrf-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="Ac-lef2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="AcOrf-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="AcOrf-4"
/note="17577 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym: AcOrf-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="baculovirus repeated ORF"
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/db_xref="GI:559071"
                                                                                                    codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="CTX; 5590 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                             Da
                                                                                                                                          primary translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                product"
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complement(5287. .6918)
                                                                                                                                                                                                                                                    complement (7899. .8921)
/gene="AcOrf-11"
                                                                                                                                                                                                                                                                                                 complement (7899. .8921)
/gene="AcOrf-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="61K; vp78; required for
primary translation product"
                                                                                                                               /product="AcOrf-11 peptide"
/protein_id="AAA66641.1"
/db_xref="GI:559080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="protein kinase"
/protein_id="AAA66640.1"
/db_xref="GI:559079"
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                                                                                                                                                                                                              codon start=1/
                                                                                                                                                                                                                          note="40093 Da primary translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="PK1; 31978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="synonym: AcOrf-10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Ac-pk-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="AC-ORF1629"
/note="61"
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4520. .5257
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1520. .5257
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db_xref="GI:559077"
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/translation="MSLAAKLIIYNYYAKYNEVHDVYGESYHHYRIVQEYLSESYVNG
MSCIERDVTAMRRLKSGSCTEPBAVKNIDAGDSIKSLSHWESTSETMGIDDNVREVLE
QIDAVVPVSYNYONGMGIFSLHNFEREISODMIDLICIGIICHREEYFMLMKKLIRIAN
FNPNNDVVGMWYNKFCVVTYVHRIMYRSVPAELVPRLSEAVKKFIRLRKSDYDDRLHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mattnatlQTLVQFYENCKNVKTRYKIINGRFGKISILSHKPTS
KLYLQKTISAHNFNADEIKVHQLMSDHPNFIKIYFNHGSINNQVIVMDYIDCPDLFET
LQIKGELSYQLVSNIIRQLCEALNDLHKHNFIHNDIKLENVLYFEALDRVYVCDYGLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLNSMKRRQQYNDIGVLKHVRNVNARDFVYCLTRYNIDCRLTNYKQIIKHEFLS"
DESYNCPRVIAEMYGRFCGIGKEHFSKHKLSCMHILFQYLRGKTTQEEKSFPCYRVIK
                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name="hrla"
/note="2 copies of 30 bp imperfect palindromic sequence"
/function="enhancer; replication origin"
/rpt_type=dispersed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARLLLQDLAS FVALSENPLDS PA I GSEKQPL FETNRNL FYKS I EDL I FKFRYKDAENH
LIFALTYH FKDYKFNELLKYVQQLS VNQQRTESSA"
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BILLEVSLVFKVKEFAPDAPLFTGPAY"
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MEDSFPIVNDQEVMDVFLVVNMRPTRPNRCYKFLAQHALRCDPDYVPHDVIRIVEPSW
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/product="major occlusion body protein"
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Arif,B.M.
                                           Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2E5,
                                                                                                                                                                                  Lauzon, H.A., Jamieson, P.B., Krell, P.J. a
Gene organization and sequencing of the
defective nucleopolyhedrovirus genome
J. Gen. Virol. 86 (PT 4), 945-961 (2005)
                                                                                                                                                                                                                                                                                                                                                               4 (bases 1 to 131160)
Li,X., Barrett,J., Pang,A., Klose,R.,
Characterization of an overexpressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CfMNPV and CfDEFNPV J. Gen. Virol. 80 (PT 7), 1833-1840 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The putative LEF-1 proteins from two distinct Choristoneura fumiferana multiple nucleopolyhedroviruses share domain home eukaryotic primases eukaryotic primases (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 11500 to 13512)
Barrett, J.W., Krell, P.J. and Arif, B.M.
Characterization, sequencing and phylogeny of the ecdysteroid UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis viruses isolated from Choristoneura fumferana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choristoneura fumiferana DEF MNPV (CfDEFNPV)
Choristoneura fumiferana DEF MNPV
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Choristoneura fumiferana defective
                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                     baculovirus infection
                                                                                                              Lauzon, H.A.M.,
                                                                                                                                                                 15784888
                                                                                                                                                                                                                                                                                                       10683327
                                                                                                                                                                                                                                                                                                                           Virology 268 (1), 56-67 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                            10423153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barrett, J.W., Lauzon, H.A., Mercuri, P.S., Krell, P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGC 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gen. Virol. 76 (PT 10), 2447-2456 (1995)
                                                                                                                                         (bases 1 to 131160)
                                                                                                                                                                                                                                                                             (bases 1 to 131160)
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  (bases 1 to 131160)
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X., Lauzon, H.A., Sohi, S.S.,
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                                                                                                              Jamieson, P.B., Krell, P.J. and Arif, B.M.
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                                                                                                                                                                                                                                                       and Arif, B.M.
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Direct Submission
Submitted (21-JAN-2005) Molecular Virology, Great Lakes Forestry
Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2E5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence update by submitter On Jan 21, 2005 this sequence Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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EILIEWSLVFKVKEFAEDAPLETGPAY"
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PETTQAFVABSPPPAQAFVAPSPPPAQAFVAPSPPPAQAFTARSPGPTFVAPPSPPPAQAFVAPSPPPAQAFVAPSPPAQAFTARSPGPTFVAPPSPQFT
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complement (1247...1858)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1. .738)
/note="ORF 1; ph Op3/Ac8; major occlusion body protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Choristoneura fumiferana
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                                                                                      note="ORF 5; Op8/Ac4"
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                                                                                                                                                                                                                                                          codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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SGS

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repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location similar to Ac hrla"

/function="enhancer; replication origin"

/complement(6723. .7871)

/note="ORF 10; Op20/Ac20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPTIKLDGWWYNKFCYLTYMYRIIRGTVPAELITRLQNVVTKYIKPEYDESNNALAMG
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NYLEDLLKRHVRR"
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/note="ORF 8; ptp-1 Op10/Ac1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (3686..4168)
/note="ORF 7; ptp-2 Op9"
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HRFGFLDRNALVEACMAVNVQVYVPDGTIRLNFKTIYFRVCQKCHAVADVPAFDDHSI
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SGC

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110 CCAACTTTTTTGCACTGCAAAAAAACACGCTTTTGCACGCGG-GCCCATACATAGTACAA

Matches 137;

Conservative

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Mismatches

26;

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Gaps

2

168

CDS

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JOURNAL
REFERENCE
AUTHORS
TITLE
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SOURCE
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AUTHORS
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Query Match
Best Local Similarity
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Antheraea pernyi nucleopolyhedrovirus
Virises; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-DEC-2004) Insect Pathology, The Sericultural Institute Caas, Sibaidu, Zhenjiang, Jiangsu 212018, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xia, A., Li, J., Li, W., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xia,A., Li,W., Mu,Z., Li,J., Zhou,Q. and Zhang,Z. Cloning and analysis of occlusion-derived virus envelope-56 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antheraea pernyi nuclear polyhedrosis virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATAC
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                                                                           VDNVPDAGFHVKRTRGDAVKQNFPETNVRSADGVDRALQQNPRLINTYLQGAKTAGVGV
LLAGGAYLAFSAATLVQDIINALNNTGGSYYVRGSNGGETAEACLLLSRTCRRDPNMN
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                                                                                                                                                                                                                   /product="occlusion-derived virus envelope-56 protein"
/protein_id="AAW48304.1"
/db_xref="GI:57233515"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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CVYRHDFVKKCVGCRMEVRHDEPTVFNQNQCALIMMVMMTAVLQFWNMYVQRKEMRYK
PTPVKTLYFESAPLKEQDTADEEEEQQSSFRWLEIISEPRVQFQFPESSSLDRLSSPP
                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                   /note="ODV-E56"
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                                                                                                                                                                                                                                                                                                                                                                                                 country="China"
  17.4%;
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80.6%;
Score 98.4; DB 10
Pred. No. 2.5e-22;
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Pred. No. 9.2e-23;
Mismatches 30;
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Search o Job time	pb Qy	Qy da	망
Search completed: June 15, 2006, 19:57:54 Job time : 4072.26 secs	229 ACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGT 272	169 ACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAAT 228	

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Maximum
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1: geneseqn198
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Aav62487 O. pseudo
Adq48575 OpiE2 pro
Aal61306 p2ZOp2F e
Adq48539 Viral vec
Aat136305 ACNPV ORF
Aat13635 ACNPV Gen
Add51646 BMNPV gen
Add51646 BMNPV gen
Add48576 Viral vec
Abz10059 Haematopo
Aas46501 Tumour su
Ade84121 Human lym
Abz10205 Haematopo
Ade84197 Human lym
Abz10205 Haematopo
Ade84197 Human lym
Abz10308 Rice stre
Ada71938 Rice gene
Abd68115 Listeria
Abd70339 Listeria
Abd70339 Listeria
Abd70339 Listeria
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Expression vectors for transforming insect cells from disparate lines useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins.

WPI; 1998-557129/47. Grigliatti TA, 27-MAR-1997; 28-JAN-1998; 26-MAR-1998;

97US-0049946P. 98CA-02221819. 98WO-CA000282

(UYBR-) UNIV BRITISH COLUMBIA.

Theilmann DA,

Pfeifer TA,

Hegedus

B

This represents a Orgyia pseudotsugata multicapsid nucleopolyhedrosis

Claim 10; Page 82; 121pp; English.

ALIGNMENTS

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RESULT 1
AAV62487
ID AAV6
XX AAV6
XX AAV6
AC AAV6
DT 17-0
DT 19-J
XX Orgy
XW Orgy
XW Op in
XX inme
KW ion
OS Orgy
XX Orgy
XX Orgy
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PN WO98
XX Orgy
XX ION
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RESULT 2
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AC ADQ4
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    ADQ48575
                                            ADQ48575 standard;
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                                                                                                                                                                                                                        The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination the integration of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpIE2 promoter that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecule comprising all or a portion of one or moviral genome and further comprising two or more recombination sites do not substantially recombine with each other, useful as gene there
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26-JUL-2002; 2002US-0398617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression gene therapy vector; ds; OpIE2 promoter.
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
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(BENN/)
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WELCH P J.
HARWOOD S.
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BENNETT R P.
WELCH P J.
HARWOOD S.
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CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                   560 BP;
                                       TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCAACCTTTTTT
                                                                                          CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 16;
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                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence
                                                                                                                                                                                                   144 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  555pp;
                                                                                                                                              97.2%; Score 548; DB 12; 1 100.0%; Pred. No. 2.1e-167; tive 0; Mismatches 0;
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                                                                                                                                                                                                   C; 116
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                                                                                                                                                                                                   G; 144 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Madden K,
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The invention relates to immunogenic analogues of multimeric proteins such as immunogenic variants of interleukin 5 (ILS) and tumour necrosis factor alpha (TNP, TNPalpha) and methods for production of immunogenic
                                                                                                                                New immunogenic analogue of a polymeric protein, useful for preparing composition for treating inflammatory diseases e.g. arthritis.
                                                                                                                                                                                                                                                                                         (BRAT/)
(VOLD/)
(MOUR/)
                                                                                                                                                                                                                                                                                                                                                           (PHAR-)
(KLYS/)
(NIEL/)
                                                                                      Disclosure; Page 195-196; 196pp; English.
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16-NOV-2001; 2001US-0331575P.
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                                                                                                                                                                                                                                                                                       PHARMEXA AS.
KLYSNER S.
NIELSEN F S.
BRATT T.
VOLDBORG B.
MOURITSEN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eric protein; interleukin 5; necrosis factor alpha; gene
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Best Local Similarity
Matches 548; Conserv
                                                                                                                                                viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expr gene therapy vector; ds; plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analogues. The immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in gene therapy. The present sequence is p2KOp2F expression vector for insect cells. This sequence is used to illustrate the method of the
                                                                                                                                                                                                                                        Viral vector-related plasmid - pIB/V5-His-DEST
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Pred. No.
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19-NOV-2002;
24-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The exemplification of the invention.
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                                            GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
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; 2002US-0398617P.
; 2002US-0427231P.
; 2003US-0456496P.
; 2003US-0474940P.
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AAT13636-731 show open reading frames 13, 20, 22-30, 32, 38, 41-46, 50-60, 62-63, 66, 68-79, 81-87, 91-92, 96-98, 101-103, 106-127, 129-130, 140-146, 146, 146-150, 152 and 154 from a total of 154 ORFs identified in the Autographa californica nuclear polyhedrosis virus (AcNPV) clone 6. Each gene is numbered according to its position in the virus genome beginning at the left end of the linear map, and irrespective of its orientation. The direction of transcription is relative to that of the polyhedrin gene. Of the 154 ORFs identified it was found that some of the ORFs 27, 30, 32, 71, 86, 123, 126 and 127) are dispensable for virus replication in cell culture or insect larvae. These genes can be deleted from the genome to: (a) provide additional sites for inserting single or multiple copies of foreign genes; and (b) to reduce the size of the virus complementary strand relative to the polyhedrin gene. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Autographa californica nuclear polyhedrosis virus complete genome sequence - useful in the prodn. of vectors for enhanced heterology protein expression, such as interleukin(s), interferon(s) and
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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                    The complete nucleotide sequence of the genome of clone 6 of the baculovirus Autographa californica nuclear polyhedrosis virus (AcNPV) has been determined. The sequence is taken from the Genbank record L22658. The patent specification claims a polynucleotide selected from open reading frames (ORFs 13, 20, 22-26, 28-30, 32, 38, 41-46, 50-60, 62-63, 66, 68-79, 81-87, 91-92, 96-98, 101-103, 106-126, 129-130, 140-146, 148-150, 152 and 154 from a total of 154 ORFs identified by the patentees. See T13636-731. Expression vectors conts. the complete genomic sequence of AcNPV, with the exception that at least one non-essential ORF is disrupted or replaced are useful for the synthesis of heterologous proteins. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
relative
OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Autographa californica nuclear polyhedrosis virus complete genome sequence - useful in the prodn. of vectors for enhanced heterologous protein expression, such as interleukin(s), interferon(s) and
                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 90-186; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-087670/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Autographa californica nuclear polyhedrosis virus clone 6; disruption; non-essential gene; heterologous protein production; expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2003
03-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NATU-) NATURAL ENVIRONMENT RES
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                                                                                                                                                                                                                                                                                            Matches 121;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a Bombyx mori (silk worm) polyhedrosis virus in which open reading frame 8 (ORF 8) gene is inactivated. The inactivated orfs gene is useful for suppressing movement of silkworm and efficiently prevents the movement of a silkworm from a chamber in which it is raised The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Bombyx mori polyhedrosis virus inactivated, or its variant, useful i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bombyx mori nuclear polyhedrosis virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; SEQ ID NO 3; 53pp; Japanese
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CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGC
                                                                                    CTACAAATCGTAGACTATTTTATTAGAATAGTCTACACTGTACTATACGCTCTCAATATA
                                                                                                                     CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                         AATTTTTTTGCAATACAAAAAAGTTCGCCTATGTTTGACATATAATATACAGTACGAACT
                                                                                                                                                                                                                                        28413 BP; 8394 A; 5713 C; 5940 G; 8366 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                    Score 93.4; DB Pred. No. 1e-18;
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Pred. No. 5.2e-21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in which open reading frame gene for suppressing movement of Bombyx
                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                 Matches
                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                        The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, and are useful as gene therapy vectors. The nucleic acid of the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a recombination region of a plasmid that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-0398617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition, gene therapy vector; ds; plasmid; recombination region.
                                                                                                                                                                                                                             Sequence 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ48576 standard; DNA; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 17; 555pp; English.
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                                487 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG
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                                                                                                                                        Similarity
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     CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG
                                                                                                                 Conservative
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                                                                                                                                                                                                                          A; 36 C; 27 G; 34 T; 0 U; 1 Other;
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RESULT 9
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                                                                                   The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders cassociated with at least 1 gene and/or their regulatory regions in a CC subject. The method comprises contacting a target nucleic acid in a CC biological sample obtained from the subject with at least 1 reagent, CC which distinguishes between methylated acid. ABZ09861 to ABZ1118 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 CC represent specifically claimed nucleotide sequences from the present invention can be used: for CC invention. Oligonucleotides from the present invention can be used: for CC differentiating between healthy haematopoietic cells and proliferative CC lymphocyric leukaemia and acute myelogenous leukaemia; as probes for CC lymphocyric leukaemia and acute myelogenous leukaemia; as probes for CC lymphocyric leukaemia and acute myelogenous leukaemia; as probes for CC lymphocyric leukaemia and acute myelogenous leukaemia; as probes for CC lymphocyric leukaemia and acute myelogenous leukaemia; as probes for CC lymphocyric leukaemia and acute myelogenous leukaemia; as probes for CC lymphocyric leukaemia and acute myelogenous leukaemia; as probes for CC lymphocyric leukaemia and acute myelogenous leukaemia; as prober for the CC amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also CC be used for detecting a predisposition to, differentiation between completic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present of nationts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C, Adorjan P, Grabs, Lipscher E, Maier S, Model F,
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ation state; gene; ds.
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Mueller V,
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                                                                         treatment
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Query Match Best Local S Matches 84

Similarity

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Score 39.6; DB Pred. No. 0.16;

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Conservative

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Mismatches

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Gaps

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Sequence 6289 BP; 1680 A; 178 C; 1488 G; 2943 T;

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The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CP bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences CP complementary to (Ss). The nucleic acid may be a peptide nucleic acid may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing CP diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or cytosine methylations. The parameters may be compared to another set of cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the $33 genomic sequences constituted from tumour suppressor genes and oncogenes. Note: The sequence data for this patent did not form part of the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뭐
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2000; 2000DE-01013847.
06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-UTN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tumour suppressor tumour; CpG dinucleotide; cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-SEP-2001.
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inucleotide; single-nucleotide polymorphism; SNP;
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                               MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2a, CDKN2B, FOGSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKNIC, GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
                                                                                                                                    Claim 26;
                                                                                                                                                          reagent that dinucleotides.
                                                                                                                                                                                                                                      Burger M,
                                                                                                                                                                                                                                                                               23-NOV-2001; 2001DE-01057491.
28-DEC-2001; 2001DE-01064501.
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                                                                                                                                                                                                                                                                                                                                                                                                                 diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; lymphoid cell proliferative disorder; methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lymphoid cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                        methylated CpG dinucleotide; single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                      follicular lymphoma; diagnosis; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                   SEQ
                                                                                                                                                                   and differentiating between lymphoid cell proliferative comprises contacting a target nucleic acid with at least one hat distinguishes between methylated and non-methylated CpG
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                                                                                                                                                                                                                                      Caldwell
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                                                                                                                                  ID NO 117; 448pp; English.
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                                                                                                                                                       Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaem cytosine methylation state; gene; ds.
   The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders
                                                                                               Claim 28; SEQ ID NO 345; 117pp; English.
                                                                                                                                                                                                                                                                                       WPI; 2003-018942/01
                                                                                                                                                                                                                                                                                                                                                                                                                Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2001; 2001US-0278333P
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1, Lipscher E, Maier S, Mc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell proliferation disorder related DNA sequence #345
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53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         state; gene;
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                                                                                                                                                                                                                                                                                                                                                                                Guetig D, P, Grabs Model F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                   G, Lesche
Mueller V,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Howe A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mueller J;
                                                                                                                                                                                                                                                                                                                                                                                      Otto
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RESULT 13
ADE84157/c
ID ADE841
XX ADE84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; lymphoid cell proliferative disorder; methylation; methylated CpG dinuclectide; single nuclectide polymorphism; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated with at least 1 gene and/or their regularory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CPG which distinguishes between methylated and non-methylated CPG.
                                 WPI; 2003-457621/43
                                                                                                                                                                                                        23-NOV-2001; 2001DE-01057491.
28-DEC-2001; 2001DE-01064501.
                                                                                                                                                                                                                                                                                                                                                            30-MAY-2003
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                                                                                      Burger M,
                                                                                                                                                                                                                                                                                                  25-NOV-2002; 2002WO-EP013265
                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003044226-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      follicular lymphoma; diagnosis; prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lymphoid cell proliferative disorder gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE84197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4896
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                                                                                                                                                 EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 9289 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACGCTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTA 269
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                                                                                         Caldwell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                         Genc
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                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                            Becker
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                                                                                         Maier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derived DNA
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                                                                                            Nimmrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of patients
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP;
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RESULT 14
ACL35887
ID ACL35
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ACC ACL35
XX
DT 02-JI
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EW 86;
XX
SW 89;
XX
OTY:
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OTY:
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OS OTY:
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PN WO2
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PN WO2
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PF 21-
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PR 22-
PR 22-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC target nucleic acid in a biological sample obtained from the subject with CC at least one reagent or series of reagents that distinguish between CC methylated and non-methylated CpG dinucleotides within the target nucleic CC acid. The genes and/or their regulatory regions are preferably selected CC acid. The genes and/or their regulatory regions are preferably selected CC acid. The genes and/or their regulatory regions are preferably selected CC GRYDI, ELKI, ABLI, APC, BCI2, CDM1, CDKN1B, CDKN1B, CDKN2B, FOS, CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBI2, TGFBRZ, TP73, CDKN1C, CC GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the CpG dinucleotides within one or more the sequences, or their complements, CC for determining the cytosine methylation state and or single nucleotide CC polymorphisms (SNPs), and for differentiating at least two of the medical CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular CC differentiation between subclasses, diagnosts, prognosts, treating and/or mepresents a nucleic acid of a pretreated genomic DNA derived from the CC above mentioned genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 83
    22-JUN-2001;
24-AUG-2001;
                                                              21-JUN-2002; 2002WO-US019668
                                                                                                                                                                                 Oryza sativa
                                                                                                                                                                                                                                                                                Rice stress-regulated promoter SEQ ID NO:14450
                                                                                                                                                                                                                                                                                                                            02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9289 BP; 2515 A; 0 C; 2097 G; 4677 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least one gene and/or their regulatory regions in a subject by contacting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                           WO2003008540-A2
                                                                                                                                                                                                                      agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                       ACL35887 standard;
                                                                                                                                                                                                                                         abiotic stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7776 ATACAACTTTCCTCTCCCTATAAAAACAAAAAAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTA 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mentioned genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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  2001US-0300112P
2001US-0314662P
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       CDNA;
                                                                                                                                                                                                                                         tolerance; transgenic plant; plant; cereal;
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52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                       2000
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Pred. No. 0.63;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75;
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Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, samplefic attents of their combinations. The present sequence is the according to the company of their combinations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2000 BP; 410 A; 329 C; 253 G; 416 T; 0 U; 592 Other;
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21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is used in the exemplification of the invention
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       425
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                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                  164 CAYCTWTKYWWKMWRWRWSAWTGMSWRTCAWMBAWRWWYTSWAMRACAAWGTKTGYCRMA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 WKYRKMMWRAKAWATKYMKYMYAATTTWTTRTCACCKWKWMAWGMYGTGYRATTKWYWAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTGTTTT
                                                                                                                                                                                                                                                                                                                                                                   TGCAAAAAACACGCTTTTGCACGCGGGCCCATACATAGTACAAACTCTACGTTTCGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCAACTTTTTTGCAC
                                            WKKCYWMWSMATWTKYWWYMWYRMASKMATTKCCYCYSACAYWYRCKWYRKYWRAMGMAY
                                                                                                                                                                                                                           ACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACACATTG
                                                                                                                                                                                                                                                                                                                                          GRWCATMTRTWGTGRTTCAGWWWKCMSYMGKKCAYAYMTWRKRRWWYAGAWMTMACTYKT
     GCGCCTCCATA 435
                                                                           GGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGAC 424
                                                                                                                                                    SAAYARMRAMWMTYARCTAAMWYWMSCRYKMWKAMAAAMYMTMRRMTMACTTAAKYRMKC
                                                                                                                                                                                                                                                                 GMWYMCMKAARMMAMWWSAYYTAMMWWKTKAYWMCAGMRACMAYWWMYWWAMMWMSYWW
                                                                                                               YGACMAAMCAYAGWMTCRSTYARTWAAGMCRASGCWAAMMCRTMTYKRWYMRTRMAGWMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Briggs SP,
T, Provart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 14450; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 37.4; DB ilarity 16.0%; Pred. No. 0.49; Conservative 155; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooper B,
: N, Ricke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
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D, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for altering the an abiotic stress such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katagiri F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                            523
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RESULT 15 ADA71938/c ID ADA719

WGCYSMYCAYA 534

ADA71938

standard; DNA; 2000

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Best Local S
Matches 42
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Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterial,
illustrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-175290/17.
                   424
                                                                              364 AGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGA 423
                                                                                                           253
                                                                                                                                          304 TCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGTGAC 363
                                                                                                                                                                        313
                                                                                                                                                                                                       370 AKYWKYWYKRRGTMSWYGKSYKKKYC---TWWCYMKCMRCYRWRKMMRKKTKYSKRCYCW 314
                                                                                                                                                                                                                                                                 184 GACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACACATT
                                                                                                                                                                                                                                                                                                                              124 CTGCAAAAAAACACGCTTTTGCACGCGGGCCCATACATAGTACAAACTCTACGTTTCGTA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                       6.4%;
Similarity 11.3%;
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'B
                   CGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTC
                                                 MSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSMMYMGSCGCYTRGWKWRSKYSMCCKKY
                                                                                                             WARSSGTWSRSAAKRTYKGYSTSRRAKMMRACRMYSACRRYSRTSYYCGCSYCGSSKWKY
                                                                                                                                                                        RYATCYWCCCYRKRGWYSRRSMMRTAGKWKMRSWSRWCRSYSWYKMYKKMWKKSYYMSYG
                                                                                                                                                                                                                                                                                               CYGCKMWTYCSYGYMKWYTYMGSYKYSRCYKYMRMYMYKGWMYMMYYSAYSSYMTWYYYY 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5263; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungal or viral infection. The present sequence was used the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
                                                                                                                                                                                                                                                                                                                                                           Conservative
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5263
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                       %; Pred. No. 1.2;
169; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Score 36.2;
Pred. No. 1.
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                                        133 CSCCTKYCSYTGYYRYCKWYKYSYYKCYYCYCYWYMSYMRYMMKCMCSRSCSSWMSCAYC 74
    484 CCGCTTATCGC 494
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Search completed: June 15, 2006, 16:31:49 Job time: 608.079 secs

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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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41.4
39.6
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11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTITY_NUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                June 15, 2006, 16:32:06 ; Search time 4719.79 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-896-888A-1
                                                                                                                                                                                                                                                                            catgatgataaacaatgtat.....tgttacagcgacacaacatg 564
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                                                                                                                                                                                                                                                                                                                                                                                     gb_est1:*
gb_est3:*
gb_est4:*
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1324
758
535
578
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593
425
669
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1101
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1032
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14
                          BZ899636
DX064229
CB410241
CO384338
DN87386
CV918268
CV918268
CNS0039X
AI437474
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          BI843287
CNSOGAHP
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                                                                                                                      CL077394
BX147578
CG751412
BH517933
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                                                                                                                                                               DU436534
                                                                                                                                                                                                                       SUMMARIES
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6682.184 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96473596
      CB410241 NISC nc10
CO384338 AGENCOURT
DN873866 nad29c08
CV918268 PH005H10
AL063938 Drosophil
AI437474 fb34b06.x
BI843287 ft59f05.x
CR709617 Tetracdon
                                                                               DU436534 109841592
CL077394 CH216-145
BX147578 Danio rer
CG751412 P045-4-E0
BH51793 BOGBL87TF
NG3392 y735h10.81
BZ902838 CH240_23
BZ899636 CH240_16P
DX064229 KBrB071K0
                                                                                                                                                                       AV398660 AV398660
                                                                                                                                                                                         Description
                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
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AV398660
LOCUS
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VERSION
KEYWORDS
                          ORIGIN
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                                                                                                                                                                                                                               COMMENT
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45	44	43	42	41	40	39	38	37	36	S	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
35	35	35	35	35.2	35.2	35.2	35.2	35.4	35.4	35.4	35.6	35.6	35.6	35.6	35.6	35.6	35.6	35.6	35.6	35.8		ū	v	35.8	Ó
	6.2						6.2					6.3			6.3			6.3			6.3				
988	972	780	589	1101	1019	815	579	997	835	755	1080	803	787	764	761	665	626	613	516	1049	715	675	655	461	857
14	ø	14	N	14	N	12	œ	12	ហ	ä	14	ø	11	ø	13	13	14	13	N	13	7	N	14	11	12
CNS0067B	DN909117	AG394612	BM525801	CNSOOLOO	BG247625	CC861440	CV968528	CG020891	CK706618	AQ751255	CNS02APV	CX336435	AQ857977	DN808697	CW655793	CL742215	AG401197	CL753134	BM278655	CL510716	BE374425	BG695019	AG358704	BH757407	CG935894
AL062985 Drosophil	DN909117 57860.3 D	AG394612 Mus muscu	BM525801 sak72a09.	AL068607 Drosophil	BG247625 602359311	CC861440 NDL.122K2	CV968528 PC063E8 i	CG020891 ZMMBBc055	CK706618 ZF101-P00	AQ751255 HS 5574 B	AL188860 Tetraodon	CX336435 JGI_XZT19	AQ857977 nbeb0011D	DN808697 76814387	CW655793 OG_BBa000		AG401197 Mus muscu	CL753134 OR BBa012	As t	CL510716 SAIL 836	BE374425 601227596	BG695019 NISC_iv11	AG358704 Mus muscu	BH757407 SALK_0561	CG935894 MBEAV05TR

ALIGNMENTS

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        Email: kmita@nias.affrc.go.jp
Project='Silkworm Genome Program in MAFF, and Research for the
Proture Program in JSPS'. see 'SilkBase',
<a href="http://www.ab.au-tokyo.ac.jp/silkbase/">http://www.ab.au-tokyo.ac.jp/silkbase/</a>, for whole ESTdb.
Location/Qualifiers
1. .679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Research Group
National Institute of Agrobiological Sciences
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6120
Fax: 81-29-838-6121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S. Bombyx mori cDNA Unpublished (2000)
Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV398660 Bombyx mori ovary BmNPV infected; 6 hr after inoculation Bombyx mori cDNA clone NV060140 T3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoptera; Endopterygota; Lepidop
Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 679)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bombyx mori (domestic silkworm)
Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV398660.1 GI:6902312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV398660
                                                                                                           /tissue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 6 hr after inoculation"
/clone_lib="Bombyx mori ovary BmNPV infected; 6 hr after inoculation"
                                                                                                                                                                                                                                                                               /organism="Bombyx mori"
/mol_type="mRNA"
/db_xref="taxon:7091"
                                                                                                                                                                                                                                                          clone="NV060140"
14.4%;
71.3%;
Score 81.2; DB 1;
Pred. No. 3.1e-14;
                       Length 679
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á 밁 ş 밁

Graves, T.,

Euteleostomi;

Pipidae;

GSS 31-DEC-2003 clone

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
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DU436534/c
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Best Local S
Matches 81
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                         162 CATGCTGATCAATGAGGCATAAAGATATAATTGGTTTATAGACACATTTGTTGAAATGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107;
                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TTTTATTAGAATAGTCTACACTGTACTATACGCTCTCAATATACTACTACACTATCAACT
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                                                                                                                    1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ekirknes@tigr.org

Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCYIJTC; http://www.venterinstitute.org/).

Original Trace: 1098415929593 Trace TI: gpn||ti||918980430

Original Trace: 1098415929593 Trace TI: Spn||ti||918980430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovine BAC End Sequences from Library CHORI-243
Unpublished (2004)
Other GSSs: 1098421042324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Ewen Kirkness
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-7536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 883)
Kirkness E., Shetty, J., de Jong, P., McEwan, J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
DU436534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 184000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DU436534.1
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                                                                                                                                                                                 Similarity
                   TTTACCAAGCTTTTAAACACCACATTTATGTTTTTGAGCCTAAATCATCAGCAAATGAATT
                                                   TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTTGCATTACAAAAAAGTTCATTTTTGC 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACACATTGAACC
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ilarity 55.1%;
Conservative
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                                                                                                                                                                                                                                                   /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: The CHORI-243 sheep (M) (Ovis aries) BAC library p by Pieter de Jong's lab at CHORI http://bacpac.chori.org/library.php?id=162"
                                                                                                                                                                                                                                                                                                                               cell_type="Blood"
clone_lib="CHORI-243"
                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9940"
/clone="CH243-284G6"
                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="Texel breed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Ovis aries"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:77190412
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                                                                                                                                                              Score 41.4; DB Pred. No. 0.18; O; Mismatches
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Ovis
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                                                                                                                                                                 66;
                                                                                                                                                                 Indels
                                                                                                                                                                                                  Length 883;
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CH243-284G6
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CL077394
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Best Local
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                    ORGANISM
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                                                                                                                                                                                                                                                                                             390 ATCTGÁÁCTCTCATTATCACTCATCTATTATAACGGÁTÁATGTÁCCCCCTACTGTÁAATC
                                                                                                                                                                                                                       450 ATAACGATATTACCACTCACTGACTCCTTCTGTACCCATATAAATT
                                                                                                                                                                                                                                                                                                                             163 GTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCT
                                                                                                                                                                                                                                                                                                                                                                                                      121 GCACTGCAAAAAAACACGCTTTTGCAC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42
                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
                                                     Danio rerio genomic clone
BX147578
BX147578.1 GI:27978953
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kremitzki,C., Carter,J., McPherson,J., Warren,W., Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome Unpublished (2003)
Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH216-145B11_Sp6.1 CH216 Xenopus tropicalis genomic CH216-145B11, genomic survey sequence
                   Danio rerio
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence start: 163
High quality sequence stop: 226.
Location/Qualifiers
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 954)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CL077394
CL077394.1 GI:40533307
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                         CCAAATACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGT 268
                                                                                                                                                                                                                                                                                                                                                                    TCAACATTAAAAAAAAGGGAGTTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_ilb="CH216"
/note="Wector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db xref="taxon:8364"
/clone="CH216-145B11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .954
                                    (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.0%;
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                                                                                                      762 bp DNA line DKEY-109J14, genomic
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                                                                                                        survey sequence.
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GSS 28-JAN-2003

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Gaps

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COMMENT
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ORGANISM
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CG751412
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AUTHORS
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 TACATAGTACAAACTCTACGTTTCGTAGACTATTTTTACATAAATAGTCTACACCGTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
                                                                                                                                                                                                                                                                                                                                                                              Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 762)

Humphray, S.J., Huckle, E. and Durham, J.L.
                                                                                                                                                                           Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemarnstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371
                                                                                                                                                                                                                                                                                                               Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence 
CG751412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG751412
P045-4-E06.ya Ppa EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campus, Hinxton, Cambridgeshire, CB10 1SA, U humquery@sanger.ac.uk Unpublished This sequence was generated from the T7 end is part of the Daniokey BAC Library created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, I
                                                                                                                                                                                                                                                  Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pristionchus pacificus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG751412.1 GI:37973841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/D_rerio/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keygene. Further details:
                                                                                                                                                                                                                                                                      12884007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGTCA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACGCTCCAAATACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCG 276
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                                                                                                                                                          00497071601498
                                                                                                                                                                                                                                                                                   Genet. Genomics 269 (5), 715-722 (2003)
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                                                                                                                                      ralf.sommer@tuebingen.mpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
clone_lib="Ppa EcoRI BAC Library"
                  €
                               /mol_type="genomic DNA"
/strain="California"
                                                                   organism="Pristionchus"
                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:7955"
/clone="DKEY-109J14"
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|mol_type="genomic DNA"
                                                                                       . 1324
                _xref="taxon:54126"
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56.7%;
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Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1324 bp DNA linear GSS 24-OCT-2003 BAC Library Pristionchus pacificus genomic,
                                                                 pacificus"
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by R. Plasterk
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Plasterk and N.V
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 758)
Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOGBL87TF BOGB Brassica oleracea
survey sequence.
BH517933
BH517933.1 GI:17726023
GSS.
                                               66;
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                                                                                                                                                                                                                                                                                       Seq primer: TF
                                                                                                                                                                                                                                                                                                      DNA is from a doubled
                                                                                                                                                                                                                                                                                                                    Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                    Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                   Tel: 301-838-3523
                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chris Town
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illarity 52.1%;
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                                                                                                                    /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
                                                                                                                                                                                              /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                    /clone_lib="BOGB"
/note="Vector: pH
                                                                                                                                                                   /clone="BOGBL87"
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                                                156 ATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiase, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J. Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yz35h10.sl Morton Fetal Cochlea IMAGE:285091 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: estGwatson.wustl.edu
Email: estGwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMAGE Consortium (info@image.llnl.
Seq primer: m13 -40 forward
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llarity 49.2%;
Conservative
                                                                                                                                                                  /db_xref="GDB:3892208"
/db_xref="taxon:9606"
/clone="IMAGE:285091"
                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens'
                                                                                  Score 38.2; DB Pred. No. 1.7; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pietter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other GSSs: CH240_23B3.TV
Contact: Harris Lewin
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Plate: 23 row: B column: 3
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Fax: 217 244 5617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: h-lewin@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bachman, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larkin, D.M.,
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
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/cell type="Blood"
/celne lib="CHORI-240"
/clone lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2:
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; S
                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                              clone="CH240_23B3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 (8), 1966-1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414
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6.7%;

Score 38; Pred. No.

DB 12; 2.1;

Length 578

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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BZ899636
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
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(http://www.chori.org/bacpac/ordering_information.htm). This work
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Consortium (IBBMC) by by University of Illinois at Urbana
Champaign, USA with funds provided by grant No. AG202-34480-11828
from USDA-CSRESS and AG99-35205-8534 from USDA/NRI (Livestock
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Plate: 16 row: P column: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome sequence
Genome Res. 13 (8), 1966-1972 (2003)
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Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., S

Bachman,S., Green,C., Wright,C.L., Campos,B.J., E

Edwards,J., Liu,L., Osoegawa,K., Womack,J.E., de
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CH240_16P5.TV CHORI-240
genomic survey sequence.
BZ899636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Harris Lewin
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT 120
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38: BAC ends.
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                                              /clone lib="CHORI-240"
/clone lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mbo
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mbo
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
                                                                                                                                                                          /sex="Male"
                                                                                                                                                                                             clone="CH240_16P5"
                                                                                                                                                                                                                                                                                         organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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    6.78;
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Benson, L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jong, P.J. and
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                                  161 TAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACG 220
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                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Spermatophyta; Magnollophyta; eudicotyledons;
Spermatophyta; Magnollophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
DX064229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institute of Agricultural Biotechnology 25 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
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GSS.
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Beom-Seok Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subsp. pekinensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DX064229
CGATTTCAACTTAATTATAATTAGAAAAACTACACAAATTTTTTAAAACGTGTTTAAAT 158
                                                                                                      TCCCCACCACCAACTTTTTTGCACTGCAAAAAAAACACGCTTTTGCACGCGGGCCCATACA
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                                                                    TCCACCACATCAATTTAGTTCGTCTCAAATAGAATCCGAATAATTGATCAGTGCCAAATA
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                                                                                                                                              Conservative
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                                                                                                                                                                                                                                /lab_host="E.coli DH10B"
/clone lib="KBTB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC!, Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                          /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB071K09"
                                                                                                                                                                                                                                                                                                                                                                               /organism="Brassica rapa subsp.
/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics Team
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genomic clone
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                                                                                                                                                            Score 37.6;
Pred. No. 2.
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BamHI BAC library Brassica rapa
KBrB071K09, genomic survey
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CB410241
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                                                                                                                                                                              175 CGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTA
                                                           186
                                                                                                  235 CCACACATTGAACCTTTT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 CTACATTGÁCTATAACAGAAATTAATCAATTATTAACAAGATAAAACGACGT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
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Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation:

cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

cDNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425 bp NISC nc10d09.x1 COGENE 6E MAX Homo 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: LLAM12849 row: G column: 18
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: LLAM12849
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                          TTTTTGATGCAATATATTTGCCAAAAAAACTCAGCTTTTATTTTCCATTTTAAACAACTA
                                                                                                                                                                                                                     TTTTTTCCAAAAGGAAAAAATTTTTTTCCTCGGGGTTTTATCCACTGTCAATACTGTA 125
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                                                           CAATATTTACAAGCTGTT 203
                                                                                                                                                                                                                                                   (bases 1 to 425)
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="COGENE 6E MAX"
/note="Vector: pAMP1; cDNA primed using oligo-dT primer,
/note="Vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMP1. Size
selected for insert sizes ranging from 0.2-1.8 kb.
Normalized to Cot5. Primary library, non-amplified.
Library constructed by M. Lovett. For more information on
this library, please contact R. Tidwell (Washington
University) or visit the COGENE website at
                                                                                                                                                                                                                                                                                                                                                                                                        http://hg.wustl.edu/COGENE/."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="maxilla, pooled"
/dev_stage="6 weeks postconception"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:5776553"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l_type="mRNA"
_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                       54.34;
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                                                                                                                                                                                                                                                                                                      Score 37.2; DB 4;
Pred. No. 3.4;
0; Mismatches 63;
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                                                                                                                                                                                                                                                                                                        63; Indels
                                                                                                                                                                                                                                                                                                                                               Length 425;
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                   164
                                                       213 TGTATACGCTCCAAATACACTACCACACATTGAACCTTTTTTGCAGTGCAAAAAA 266
                                                                                                  104 CCAATAAATAGGGGAACCTTCTGGTATAGTTGTAAAGAATACATCCAATGTATGCAACGT
                                                                                                                                        153 CCCATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGT 212
                                                                                                                                                                                                    Similarity
                   Conservative
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6.6**%**;

0;

Score 37.2; DI Pred. No. 3.8; 0; Mismatches

. 8 DB 8; 48;

Length 669; Indels

0

Gaps

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CO384338
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lead through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMM15322 row: column: 11
High quality sequence stop: 534.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Bruce Blumberg
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Xenopus laevis
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                   /clone lib="Blumberg_Cho dorsal blastopore lip"
/clone = "Organ: embryo; Vector: pBluescript SK:; Site_1:
/note="Organ: embryo; Vector: pBluescript SK: site_1:
EcoRI; Site_2: KhoI; Library was prepared from 50 ug of
total RNA by oligo-df priming and AMV reverse
transcriptase. After addition of EcoRI linkers and
EcoRI-XhoI digestion, the cDNA was size selected by
chromatography on Sepharose CL-4B columns and fractions
containing cDNAs larger than 500 bp were ligated into
EcoRI XhoI-digested lambda ZAPII (UniZAP-XR) and packaged
in vitro. Average insert size is 1.4 kb. The original
library contained 6 x 106 recombinants, of which 3 x 106
were amplified and stored at -70 C in sM buffer containing
phagemids used to infect Top10F. References: Science 253,
196-196 and Methods in Molecular Biology 97, 555-574.
Additional sequences from this library have been deposited
under the name Xenopus laevis dorsal blastopore lip.
Library constructed by Bruce Blumberg (University of
California, Irvine, Department of Developmental and Cell
California,
Biology)."
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/mol_type="mRNA"
/db_xref="taxon:8355"
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DN873866
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                                                                                                                                                                                                                                                        315 CACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGTGACAGGACGCCAGC
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nad29c08.yl Dog eye
cDNA clone nad29c08
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Plate: 29 row: c column: 08
Seq primer: Universal M13 Reverse.
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Unpublished (2005)
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Fax: 301 496 0078
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Mammalia; Eutheria;
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                                                                                                                                                                       TTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCAT
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                                                                                                                                                                                                                                                                                               6.6%;
llarity 50.3%;
Conservative
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NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                      carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCC(T)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC). Analyzed data available through http://neibank.nei.nih.gov."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Dog eye cornea. Unnormalized (nad)"
/note="Organ: Bye; Vector: pCMVSport6; RNA was extracted
from dog cornea tissue. A directionally cloned cDNA
library in the pCMVSpORT6 vector (Invitrogen) was
constructed at Bioserve Biotechnology (Laurel MD)
constructed at Bioserve Biotechnology (Laurel MD)
plasmid System, full details of which are contained in th
manufacturer's Instruction manual
(http://www.lifetech.com/). First strand synthesis was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Cornea"
/dev_stage="Adult"
/lab_host="EMDH10B"
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/mol_type="mRNA"
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                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1101)
                                                                                                                                                                              AL063938 1 GI:4941795 GSS
                                                                                                                                                                                                                                         DNA linear GSS 03-Ju Drosophila melanogaster genome survey sequence T7 end of BAC BACR08012 of RPCI-98 library from Drosophila melanogaster (fly), genomic survey semisore
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Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van Weet,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T. and Judelson, H.S.
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CV918268
Submitted (02-JUN-1999) Genoscope -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: howard.judelson@ucr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Plant Pathology University of California Webber Hall, Riverside, CA 92521, Tel: 909 787 4199
Fax: 909 787 4294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Judelson HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Large-scale gene discovery in the oomycete Phytophthora infestans reveals likely components of phytopathogenicity shared with true
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Phytophthora infestans
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/mol_type="mRNA"
/strain="88069"
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55.1%;
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"Vector: pSPORT1"
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Pred. No. 5;
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Search completed: June 15, 2006, 18:15:40 Job time: 4724.79 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila NA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

1 101
                                                                                                                                                                                                                                                                      1008 CMCACYYAYWCACAAMCCMTCCCCTCTCTATAATAACATCTAATAATCATWAAAYTACMAH
                                                                                                                                                                                                                                                                                                                                                                                                        1068 CAMINMATMACACACATAYATCTCTCMIMCIMYACAMACAAAIMWACTAYWCACIMIAYA 1009
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                                                                                                                                     948 MAMAAWAWATAWCWMAYHMTMTCACACACWCACTATACWCWWACCYACWT 899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR08012"
/clone_lib="RPCI-98"
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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1 EMC Celerra SIDS3/ptodata/2/ina/5 COMB.seq:*

2: /EMC Celerra SIDS3/ptodata/2/ina/6A COMB.seq:*

3: /EMC Celerra SIDS3/ptodata/2/ina/6A COMB.seq:*

4: /EMC Celerra SIDS3/ptodata/2/ina/6A COMB.seq:*

5: /EMC Celerra SIDS3/ptodata/2/ina/H COMB.seq:*

6: /EMC Celerra SIDS3/ptodata/2/ina/H COMB.seq:*

7: /EMC Celerra SIDS3/ptodata/2/ina/PCOMB.seq:*

8: /EMC Celerra SIDS3/ptodata/2/ina/PCOMB.seq:*

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10: /EMC Celerra SIDS3/ptodata/2/ina/BCOMB.seq:*
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5458.628 Million cell updates/sec
                 Sequence 89, Appl Sequence 1, Appli Sequence 1, Appli Sequence 25113, A Sequence 103819, Sequence 103821, Sequence 103863, Sequence 103864, Sequence 160230, Sequence 160231, Sequence 160231, Sequence 160232, Sequence 160232, Sequence 160274, Sequence 160274, Sequence 160276, Sequence 16227, A Sequence 14629, A Sequence 14629, A Sequence 14629, A Sequence 16227, A Sequence 16228, A
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Sequence 89, App
  160276,
14619, A
14620, A
16227, A
16228, A
12642, A
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APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
IIILE OF INVENTION: ESTS and Encoded Human P
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15639
LENGTH: 505
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; ORGANISM: Homo sapiens
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Sequence 15639, Application
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                                                            RKMYYMWKYWMWSWWCYRMGAAMYGMSARAYRMYASMSACKMCSRMMKMMSWSMWMRCWR
                                                                                                    GACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG
                                                                                                                                           SCRGTCAKMWRYARYAKRYASSMGKYMMGCRWCYAKCARMYGYYRSRSRSTGSRGMKYRR
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Result No. ۵ :

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US-09-621-976-15639
US-09-621-011-89
US-09-621-011-89
US-09-627-0767-25113
US-09-270-767-25113
US-09-249-016-103820
US-09-949-016-103821
US-09-949-016-103821
US-09-949-016-103864
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US-09-949-016-160278

Database :

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB Maximum DB

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length: 0 length: 2000000000

Total number of hits satisfying chosen parameters:

1403666 segs, 935554401 residues

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Title: Perfect score:

US-09-896-888A-1 564 1 catgatgataaaca

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OM nucleic - nucleic search, using sw model

Copyright

GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration

June 15, 2006, 16:32:43 ; Search time 193.328 Seconds

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RESULT 2
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Patent No. 6590075
GENERAL INFORMATION:
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EARLIER APPLICATION NUMBER: PCT
EARLIER FILING DATE: 1998-03-06
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R APPLICATION NUMBER: 60/047,615
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APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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APPLICATION 1
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APPLICATION NUMBER: 60/047,618
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APPLICATION NUMBER: 60/047,583
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APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/043,580 APPLICATION NUMBER: 6
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 89
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Patent No. 6878687
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (103)
                                              ZIP: 19426
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PEOOLP1
CURRENT APPLICATION NUMBER: US/09/621,011
CURRENT FILING DATE: 2000-07-20
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APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 536
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500 Arcola Rd. 3C43
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                                                                                                                                                                                                                                                                                                  GALANIN RECEPTOR, TRANSFORMED CELLS
                                                                  Release #1.0, Version #1.30
                               US/08/693,308
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Pred. No. 0.41;
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AND USES THER
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

17-FEB-1994

FR 94/01808

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; Sequence 25113, Application US/09270767
; Patent No. 6703491
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US-09-270-767-25113
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                                                                                                                   Best
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SEQ ID NO 25113
LENGTH: 902
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Best Local Similarity 54.4%;
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                                                                                                                                   Query Match
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APPLICATE: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
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                                                                                                                                                                                                      TYPE: DNA
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APPLICATION NUMBER: WO PCT/FR95/00172
FILING DATE: 14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: N
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LOCATION:
                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Smith Ph.D., Julie K. REGISTRATION NUMBER: 38,619 REFERENCE/DOCKET NUMBER: ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
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265 AAGTACGTGTCGGCAGTCACGTAGGCCGGCCTTATCGGGTCGCGTCCTGT 314
                                 440 TAACTCGATGTAGCATCTCCAGATACAATTGAGCTCATAGAACTGTTTGAAAGGGAAAAT
                                                                 205 TACACCGTTGTATACGCTCCAAATACACTACCACATTGAACCTTTTTTGCAGTGCAAAA 264
                                                                                                     62;
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Pred. No. 1.1;
0; Mismatches
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Pred. No. 1.3;
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US-09-949-016-103819
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; ORGANISM: Drosophila melanogaster
US-09-270-767-9827
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US-09-270-767-9827/c
; Sequence 9827, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9827

LENGTH: 5003
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103819
LENGTH: 601
                                                                                                                                                        Matches
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Best Local Similarity
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                  Local Similarity
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523
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                                                                           GCTAAACATAGATATTTGAGACTTTTTCTTCAGGAATTATTGATCTGAAGTTGTATTTAA
                                    TGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACT 115
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Pred. No. 1.9;
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Pred. No. 2.7;
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; ORGANISM: Human
US-09-949-016-103820
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US-09-949-016-103821
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                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103821
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103820
                                                                                                                                                     Query Match
Best Local
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Patent No. 6812339
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                     Local Similarity
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                                                          102 GCTAAACATAGATATTTGAGACTTTTTCTTCAGGAATTATTGATCTGAAGTTGTATTTAA
67
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                                                                                                                              Score 32.2; DE Pred. No. 1.9; 0; Mismatches
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Pred. No. 1
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                                                                                                                                                                 Length 601;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103863
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US-09-949-016-103863
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103864
                                                                                                       Query Match
Best Local (
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                    LENGTH: 601
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133 GCTAAACATAGATATTTGAGACTTTTTCTTCAGGAATTATTGATCTGAAGTTGTATTTAA 192
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                                                                                     61;
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                                      7 GATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTGTTTTCA 66
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                                                                                                          Similarity
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Pred. No. 1.9;
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Pred. No. 1.
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OF DETECTION
                                                                                                                          Length 601,
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                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-160230
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US-09-949-016-103865
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US-09-949-016-103865
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16230
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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SEQ ID NO 103865
LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                    Query Match
Best Local Similarity
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Best Local Similarity
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  Matches
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                                                                                                                                                   LENGTH: 601
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/241,755
FILING DATE: 2000-10-20
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Conservative
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                    56.0%;
Score 32.2; Di
Pred. No. 1.9;
0; Mismatches
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Pred. No. 1.9;
0; Mismatches
                                        DB 3; Length 601;
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                                            ; ORGANISM: Human
US-09-949-016-160232
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 160231
                                                                                                                NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 160232
LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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Best Local Similarity
  Query Match
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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PRIOR FILING DATE: 2000-09-08
                                                                                              TYPE: DNA
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5.78;
  Score 32.2;
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Search Job tim	Db	Ą	Ф	ş	Best Match
Search completed: June 15, 2006, 17:18:09 Job time : 195.328 secs	162 TCTATCAGAATATGCTCTTTTCTAATCCATTGGTTCCCCATCTCAGATT 210	67 TGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACT 115	102 GCTAAACATAGATATTTGAGACTTTTTCTTCAGGAATTATTGATCTGAAGTTGTATTTAA 161	7 GATAAACAATGTATGGTGCTAATGTTGCTTCAACAACTACTGTTGAACTGTGTTTTCA 66	Best Local Similarity 56.0%; Pred. No. 1.9; Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*

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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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US-10-622-088-126
US-10-846-911-60
US-10-846-911-60
US-10-899-107-60
US-10-899-107-60
US-10-622-088-814
US-10-622-088-149
US-09-896-888A-15
US-09-896-888A-15
US-09-896-888A-15
US-10-473-126-345
US-10-473-126-345
US-10-398-221-11528
US-10-398-221-11528
US-09-991-876-89
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                   Sequence 1, Appli
Sequence 60, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 89, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 223, Appl
Sequence 233, Appl
Sequence 1528, Appl
Sequence 3152, Appl
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5148,	ຶທ	e 917		Sequence 2215, Ap		Sequence 559402,		Sequence 1462, Ap			Sequence 1463, Ap	Sequence 783595,	e 1701		Sequence 68947, A		Sequence 129121,	27884,	27884,		6450,	2179,	e 2178,	Sequence 26311, A			Sequence 89, Appl

ALIGNMENTS

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Sequence 1, Application US/09896888A

Patent No. US20020116723A1

GENERAL INFORMATION:
APPLICANT: The University of British Columbia
FILE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/896,888A

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US/09/048,911

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/049,946

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 1

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Best Local Similarity 100.0%; Pred. No. 4.8e-175;
Matches 564; Conservative 0; Mismatches 0;
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ORGANISM: Orgyia
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GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
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CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/USO3/22437
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-17-26
PRIOR PRIOR PLICATION NUMBER: US 60/427,231
PRIOR FILING DATE: 2002-11-19
PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR APPLICATION NUMBER: US 60/474,940
PRIOR FILING DATE: 2003-03-24
PRIOR FILING DATE: 2003-03-26
PRIOR FILING DATE: 2003-06-03
                                                                                            Query Match
Best Local Similarity
Matches 548; Conserv
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SEQ ID NO 126
LENGTH: 560
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 126, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J. APPLICANT: Harwood, Steven
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
                                                                                                                                                                                   ORGANISM: Unknown FEATURE:
                                                                                                                                                                    OTHER INFORMATION: OpIE2 promoter sequence
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   TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCCACCAACCTTTTTT 120
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Madden, Knut
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                                                                                             Conservative
                                                                                                          97.2%; Score 548; DB 9; L
100.0%; Pred. No. 9.2e-170;
                                                                                            0; Mismatches
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CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 2773
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (625)..(630)
                                            LOCATION: (593)..(598)
OTHER INFORMATION: BamHI
                                                                                                                                                                                   NAME/KEY: misc recomb LOCATION: (573)..(578)
                                                                                                          OTHER INFORMATION: ECORI
                                                                                                                          NAME/KEY: misc_recomb
LOCATION: (586)..(591
                                                                                                                                                       FEATURE:
                                                                                                                                                                     OTHER INFORMATION: AvaI site
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                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial sequence
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                                               Bite
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Sequence 60, Application US/10295074
Publication No. US20030185845A1
GENERAL INFORMATION:
APPLICANT: Pharmexa A/S
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS
FILE REFERENCE: P1013DK00
FEATURE: OTHER INFORMATION: p2ZOp2F expression vector
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OTHER INFORMATION: ApaLI site US-10-295-074-60
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Best Local Similarity
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LOCATION: (2294)..(2299)
OTHER INFORMATION: AVAI, SmaI,
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NAME/KEY: misc_recomb
LOCATION: (2284)...(2289)
OTHER INFORMATION: Aval site
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LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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LOCATION: (2551)..(25
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI site
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LOCATION: (1156)..(1161)
OTHER_INFORMATION: ApaLI site
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                                                             GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
                                                                                                                             GGACGCCCCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC
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US-10-846-911-60
; Sequence 60, App
; Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KLYSNER, Steen APPLICANT: NIELSEN, Finn Stausholm
                                    NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: AvaI site
                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_recomb
LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc recomb LOCATION: (573)...(578) OTHER INFORMATION: AVAI
                                                                                        NAME/KEY: misc recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI
FEATURE:
                                                                                                                                                                               FEATURE: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PStI
                                                                                                                                                                                                                                                  LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
                                                                                                                                                                                                                                                                      NAME/KEY: misc_recomb
LOCATION: (1156)..(11
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LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
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LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
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NAME/KEY: misc_recomb
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LOCATION: (593)..(598)
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Sequence 60, Application US/10939107

publication No. US20050180947A1

GENERAL INFORMATION:
APPLICANT: Pedersen, Hans Rudolf
APPLICANT: Ebert, Bjarke
APPLICANT: Ebert, Bjarke
APPLICANT: Rasmussen, Peter Birk
ITILE OF INVENTION: Novel Application of Vaccination Aga
FILE REFERENCE: 674542-2020

CURRENT APPLICATION NUMBER: US/10/939,107

CURRENT APPLICATION NUMBER: PCT/DK03/00147

PRIOR APPLICATION NUMBER: 60/363,128

PRIOR FILING DATE: 2002-03-11

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin version 3.1
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; OTHER INFORMATION: AVAI, SmaI, FEATURE:
; FEATURE: misc_recomb
; LOCATION: (2551)..(2556)
; OTHER INFORMATION: ApaLI site
US-10-846-911-60
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US-10-939-107-60
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Best Local Similarity
Matches 548; Conserv
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100.0%; Pred. No. 1
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; OTHER INFORMATION: ApaLI site US-10-939-107-60
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Best Local Similarity
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NAME/KEY: misc recomb

LOCATION: (1156)..(1161)

OTHER INFORMATION: Aball (
FEATURE:
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NAME/KEY: misc_recomb
TOCATION: (593)...(598
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LOCATION: (2294)..(2299)
OTHER INFORMATION: AvaI,
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OTHER INFORMATION: HindIII site
FEATURE:
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TYPE: DNA
ORGANISM: Artificial sequence
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LOCATION: (2551)..(25
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: AvaI
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI
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OTHER INFORMATION: BamHI
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LOCATION: (586)..(591)
OTHER INFORMATION: ECORI
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LOCATION: (573)..(578)
OTHER INFORMATION: AvaI
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LOCATION: (561)..(566
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LOCATION: (629)..(634)
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                                                               181 GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
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                                                                                                        65 TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
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                                                                                                                         TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCAACCTTTTTT
                                                CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US FOT/US03/22437
PRIOR FILING DATE: 2003-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR PILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-11-19
PRIOR PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR PILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-24
PRIOR FILING DATE: 2003-03-24
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US-10-622-088-89
                                                                                                                                                                                       US-10-622-088-89
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 89
LENGTH: 5038
TYPE: NAME
                                                                                                          Query Match
Best Local Similarity
Matches 547; Conservat
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APPLICANT: Bennett, Robert P.
APPLICANT: Welch, Peter J.
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Publication No.
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/474,940 PRIOR FILING DATE: 2003-06-03
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                                                                                                                                                                                                      OTHER INFORMATION: pIB/V5-His-DEST
                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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                                 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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Madden, Knut
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                                                                                                            Conservative
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                                                                                                                           96.98;
                                                                                                          Score 546.4; DB 9;
Pred. No. 9.2e-169;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09896888A

Patent No. US20020116723A1

GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-4

CURRENT APPLICATION NUMBER: US/09/896,888A

CURRENT FILING DATE: 2001-6-29

PRIOR APPLICATION NUMBER: US/09/048,911

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-27

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver: 2.0

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 14

LENCTH: 462

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE: TUROREMETTON DESCRIPTION OF SEQ ID NO 14
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Best Local Similarity
Matches 462; Conserv
                                     162 AGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGC 221
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                                                                                                                                                             81.9%;
ilarity 100.0%;
Conservative
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                                                                                                                                                                           Score 462; DB 3; Li
Pred. No. 2.1e-141;
                                                                                                                                                               Mismatches
                                                                                                                                                             0,
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APPLICANT: Madden, Nature APPLICANT: Frimpong, Kenneth APPLICANT: Frimpong, Kenneth E. APPLICANT: Franke, Kenneth E. TITLE OF INVENTION: Viral Vectors Containing Rec FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT APPLICATION NUMBER: US/03/22437
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2003-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/396,617
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR APPLICATION NUMBER: US 60/474,946
PRIOR APPLICATION NUMBER: US 60/474,946
PRIOR FILING DATE: 2003-03-24
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin version 3.2
SEQ ID NO 127
LENGTH: 147
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                   NAME/KEY: misc_feature; LOCATION: (141)..(148)
COTHER INFORMATION: n may be any nucleotide
US-10-622-088-127
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APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Madden, Knut
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
                                                                                   Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Recombination
                                                                                                                                                                                                                                                     FEATURE:
    487 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTAAACACAGTTGAACAGCATCTGTTACAGCGACACAACAT 462
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D. US20040219516A1
                                                                                 11.0%; Scillarity 100.0%; P. Conservative 0;
                                                                                   Score 62; DB; Pred. No. 1.7
0; Mismatches
                                                                                                                                                                                                                                                                    region of pIB/V5-His-DEST
                                                                                                      DB 9; Lo
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                                                                                                                         Length 147
                                                                                      Indels
                                                                                   Gaps
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      CURRENT APPLICATION NUMBER: US/09/896,888A CURRENT FILING DATE: 2001-06-29
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RESULT 9
US-10-622-088-149
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                                                         Sequence 16, Application US/09896888A Patent No. US20020116723A1
GENERAL INFORMATION:
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APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/474,940
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PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
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APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

NAME/KEY: misc_feature
LOCATION: (141)..(142)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: CDS
LOCATION: (145)..(276)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Recombination region of pIB/V5 His DEST
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Madden, Knut
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100.0%; Pred. No.
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PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16
LENGTH: 92
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                RESULT 12
US-10-473-126-199/c
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US-09-896-888A-15
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Sequence 199, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 15
LENGTH: 88
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. US20020116723A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Insect Expression Vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: The University of British Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Fragment of OTHER INFORMATION: promoter sequence of the ACMNPV ien gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Fragment OTHER INFORMATION: promoter sequence of the ACMNPV ien gene
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                                                                                                                                                                                                               172
                                                                                                                                                                                                                                                                       186 CTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACACATTGA
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                                                                                                                                                                                                                                                   16 AATTTTTTTGCAATGCAAAAAGTTCACTTTTGCCTGACACTCCATATACAGTACAATCT
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                                                                                                                                                                          CTACAAATCGTAG 88
                                                                                                                                                                                                               CTACGTTTCGTAG 184
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                                                                                                                                                                                                                                                                                                                                          7.6%;
74.0%;
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Pred. No. 0.0033;
0; Mismatches 1
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Pred. No. 5.9e-08
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US-10-221-714A-223
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                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
SEQ ID NO 223
LENGTH: 9289
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                                                                                                                          Matches
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CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 199
LENGTH: 6289
                                                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity 53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Diagnosis of Diseases Associated with TITLE OF INVENTION: tumor suppressor genes and oncogenes FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2003-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: proliferative disorders FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: DE 10013847.0 PRIOR FILING DATE: 2000-03-15 PRIOR APPLICATION NUMBER: DE 10019058.8 PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/EP01/02955 PRIOR FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OLEK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                              7896 AATTTATTTATATAACCAAATAAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 7837
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                                                                                                                        Conservative
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                                                                                                                                         7.0%;
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                                                                                                                    Score 39.6; Di
Pred. No. 0.32
0; Mismatches
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                                                                                                                                                            DB 8;
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RESULT 15

US-10-398-221-1528/c

Sequence 1528, Application US/10398221

Publication No. US20040018514A1

GENERAL INFORMATION:
APPLICANT: KUNST, Frederik
APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221

CURRENT APPLICATION NUMBER: PCT/FR 01/03 061

PRIOR APPLICATION NUMBER: PCT/FR 01/03 061

PRIOR FILING DATE: 2001-10-04
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CURRENT FILING DATE: 2003-09-26
INUMBER OF SEQ ID NOS: 1258
SEQ ID NO 345
LENGTH: 6289
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FOTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-345
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US-10-473-126-345/c
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APPLICANT: Epigenomics AG
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cel-
TITLE OF INVENTION: proliferative disorders
                                                                                                                                                                      PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1528
LENGTH: 986
TYPE: DNA
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Best Local Similarity 52.5%;
Matches 83; Conservative
Query Match
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                                                         NAME/KEY: misc-feature
LOCATION: (1)..(end)
OTHER INFORMATION: n can be any nucleotide
                                                                                                                                ORGANISM: Listeria monocytogenes-4B FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4896 AATTTATTTATATAACCAAATAAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 4837
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6.3%;
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Pred. No. 0.9;
0; Mismatches 75; Indels
Score 35.4;
DB 8;
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Length 986;
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Search completed: June 15, 2006, 18:02:42 Job time: 1907.88 secs

OM nucleic - nucleic search, using sw model Run on: June 15, 2006, 17:21:03; Search time 62.413 Seconds (without alignments) 2127.111 Million cell updates/sec Title: US-09-896-888A-1 Perfect score: 564 Sequence: 1 catgatgataaacaatgtattgttacagcgacacaacatg 564 Sequence: 2027 seqs, 117694381 residues Total number of hits satisfying chosen parameters: Total number of hits satisfying chosen parameters: Total number of hits satisfying chosen parameters: Searched: 20227 seqs, 117694381 residues Total number of hits satisfying chosen parameters: Searched: 20227 seqs, 117694381 residues Total number of hits satisfying chosen parameters: Seq length: 0 Maximum Match 100* Listing first 45 summaries Published Applications NA New:* 1: /EMC Celerra SID33/pcdata//jpubpna/US09_NEW pUB.seq:* 2: /EMC Celerra SID33/pcdata//jpubpna/US09_NEW pUB.seq:* 4: /EMC Celerra SID33/pcdata//jpubpna/US09_NEW pUB.seq:* 5: /EMC Celerra SID33/pcdata//jpubpna/US09_NEW pUB.seq:* 6: /EMC Celerra SID33/pcdata//jpubpna/US09_NEW pUB.seq:* 5: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 6: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 7: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 8: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 9: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 6: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 7: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 8: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 9: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 10: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 10: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 11: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 12: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 13: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 14: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 15: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 16: /EMC Celerra SID33/pcdata//jpubpna/US0_NEW pUB.seq:* 17: /EMC Celerra SID33/p
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27 28.4 5.0 2108 6 US-10-93-349-5230 28 28.4 5.0 4611 7 US-11-267-871-717 29 28.4 5.0 4611 7 US-11-267-871-717 29 28.4 5.0 4611 1 US-09-484-331-19 30 28.4 5.0 5264 6 US-10-485-397-10 31 28.4 5.0 5264 6 US-10-485-397-10 32 28.4 5.0 5314 1 US-09-484-331-27 33 28.4 5.0 5408 6 US-10-485-397-9 34 28.4 5.0 5715 7 US-11-288-392-4 35 28.4 5.0 6233 7 US-11-296-119-10 36 28.4 5.0 9737 1 US-09-484-331-22 37 28.4 5.0 9737 1 US-09-484-331-23 38 28.4 5.0 9737 1 US-09-484-331-23 38 28.4 5.0 9737 1 US-09-484-331-24 40 28.4 5.0 10060 1 US-09-484-331-24 40 28.4 5.0 10060 1 US-09-484-331-25 41 28.4 5.0 11772 7 US-11-246-405-17 6 42 28.2 5.0 1688 7 US-11-242-317-38 6 43 28.2 5.0 2416 7 US-11-249-902-18041	45			Ω							^	a	o		Ω					,
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52108 4611 7 4644 1 5244 1 5244 4 5314 1 5314 6 5233 7 6233 7 1006 7 9737 1 1007 7 1107 7	28.2	28.2	28.2	28.2	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	
6767744447764644766	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	
6 US-11-953-349-5230 7 US-11-267-871-717 1 US-99-484-331-29 1 US-99-484-331-27 6 US-10-485-397-10 1 US-99-484-331-27 6 US-11-258-392-4 7 US-11-258-392-4 7 US-11-296-119-10 1 US-99-484-331-23 1 US-99-484-331-23 1 US-99-484-331-23 1 US-99-484-331-24 1 US-99-484-331-25 1 US-99-484-331-28	3214	2416	1688	687	11772	10060	9871	9737	9737	9737	6233	5715	5408	5314	5264	5247	4644	4611	2108	
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	US-10-449-902-18041	US-11-289-102-76	US-10-449-902-10918	US-11-242-317-38	US-11-246-405-17	US-09-484-331-25	US-09-484-331-24	US-09-484-331-28	US-09-484-331-23	US-09-484-331-22	US-11-296-119-10	US-11-258-392-4	US-10-485-397-9	US-09-484-331-27	US-10-485-397-10	US-09-484-331-20	US-09-484-331-19	US-11-267-871-717	US-10-953-349-5230	CC +C
	18041, A	76, Appl	10918, A	38, Appl	17, Appl	25, Appl	24, Appl	28, Appl	23, Appl	22, Appl	10, Appl	4, Appli	9, Appli	27, Appl	10, Appl	20, Appl	19, Appl	717, App	5230, Ap	10000

ALIGNMENTS

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RESULT 1

US-10-953-349-868/c
US-10-953-349-868/c

Sequence 868, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILLE OF INVENTION HORDER: US/10/953,349

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOPTWARE: PATENTIN Version 3.3

SEQ ID NO 868

LENGTH: 1216
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-953-349-868
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US-10-449-902-9093/c
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Sequence 903, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
APPLICANT: FOUNDATION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                       125 ТБСАЛАЛАЛАСА 136
                                                                                                                                                                                                                                                                                                                                                                                                                                   232 CATTACAGCTCATCCGCATCTTTGGTTTCGATTATCTTACAAGTACCAACAACTTTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 AAGCCAAACACGGCCTTATACTACAATCCTCACTACACCCTTTCCGAAGAACTCTGCATC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 CATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCAACCTTTTTTGCAC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTTTTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70;
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ilarity 53.0%;
Conservative
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Pred. No. 0.17;
0; Mismatches 62;
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CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver: 2:1
SEQ ID NO 9093
LENGTH: 3119
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US-10-449-902-2563/c
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LENGTH: 1127
TYPE: DNA
ORGANISM: Oryza sativa
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APPLICANT: Bio-oriented Technology Research Advancement Institute APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JF 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JF 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTMARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK104298
DATABASE ENTRY DATE: 2002-08-28
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK106441
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                   218
                                                                                                                        407 TCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCG 466
                                                                                                                                                                                                        347 TGTTGTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAAC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 TTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACACATTGAACCT 249
                                        467 GACACGAGGCGCCC 480
                                                                                 158 CTCGCACCAGATCTCTCCGCCCCCCCCTCTCTCCCGCACGCGATCCGACGCGGGCGCTCG
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APPLICANT: LOOK, Maxime P.
APPLICANT: MORELER, Heinz
TITLE OF INVENTION: Method and nucleic acids for TITLE OF INVENTION: Method and nucleic acids for TITLE OF INVENTION: proliferative disorders FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
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Publication No. US20660123505A1

GENERRAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

CURRENT FILING DATE: 2003-05-29

CURRENT FILING DATE: 2003-05-29

CURRENT FILING DATE: 2003-05-29

CURRENT FILING DATE: 2003-05-29
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PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19810
LENGTH: 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 350, Application US/10517441 Publication No. US20060121467A1
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ORGANISM: OTYZA BATİVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK070153
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2002-203269 PRIOR FILING DATE: 2002-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FOEKENS, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467
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MODEL, Fabian
NIMMRICH, Inko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACACGAGGCGCCC 480
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KOENIG, Thomas
MAIER, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGACGGTGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCGCACCAGATCTCTCCGCCCCCCCCCCCTCTCTCCCGCACGCGATCCGACGCGGGCGCTCG
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SCHMITT, Manfred
                                                                                                                                                                                                                                                                                                                                 RUJAN, Tamas
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                                                                                                                                                                                        the improved treatment of breast cell
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PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 350
LENGTH: 7833
TYPE: DNA
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity
Thes 79; Conserve
                                                                                                                                                                                                                                 APPLICANT: MARX, Almuth
APPLICANT: HOBFLER, Heinz
APPLICANT: HOBFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the following proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR PILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-10-01
                                                                                         ; FEATURE:
; OTHER INFORMATION:
US-10-517-441-624
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US-10-517-441-350
                                                                                                                                                                  SEQ ID NO 624
LENGTH: 7833
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 624, Application US/10517441 Publication No. US20060121467A1
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Best Local Similarity 50.0%;
Matches 79; Conservative
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
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                                                                                                                                         ORGANISM: Artificial Sequence
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KOENIG, Thomas
MAIER, Sabine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHMITT, Armin
SCHMITT, Manfred
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                   Conservative
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                                                                                                       chemically treated genomic DNA
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                                  50.0%;
               ; Score 31.6; D; ; Pred. No. 1.2; 0; Mismatches
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Pred. No. 1.2;
0; Mismatches
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                 79;
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                 Indels
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Sequence 8, Application US/10485397

Publication No. US20060099673A1

GENERAL INFORMATION:
APPLICANT: ALTANA Pharma AG

ITITLE OF INVENTION: Novel Recombinant Gene Expression Method
FILE REFERENCE: B697USPCT01

CURRENT APPLICATION NUMBER: US/10/485,397

CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.0

SEQ ID NO 8

LENGTH: 7943

TYPE: DNA
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SOFTWARE: PATENTIN version 3.0
SEQ ID NO 7
LENGTH: 7873
TYPE: DNA
ORGANISM: Artificial
FEATURE:
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                                                                                                                                                                                                                                                                                                                                          RESULT 8
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US-10-485-397-7
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/485,397
CURRENT FILING DATE: 2004-01-30
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ORGANISM: Artificial FEATURE: OTHER INFORMATION: pGFPstopneoSECIS is a circular plasmid DNA
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45.9%;
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Pred. No. 1.5;
0; Mismatches 126;
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RESULT 10
US-10-517-441-462/c
; Sequence 462, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
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Publication No. US20060123505A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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LENGTH: 1006
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER: OF SEQ ID NOS: 56791
NUMBER: OF SEQ ID NOS: 56791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK099538
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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llarity 51.4%;
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Pred. No. 0.77;
0; Mismatches 67;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-517-441-736/c
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CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
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SEQ ID NO 462
LENGTH: 9353
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          Sequence 736, Application US/10517441 Publication No. US20060121467A1
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Best Local Similarity
                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
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TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell TITLE OF INVENTION: proliferative disorders FILE REFERENCE: 47675-93
                                                                                                                                                                        APPLICANT:
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HARBECK, Nadia
KOENIG, Thomas
MAIER, Sabine
                                          MARTENS, John
MODEL, Fabian
MODEL, Tabian
NIMMRICH, Inko
RUJAN, Tamas
SCHMITT, Armin
SCHMITT, Marnired
LOOK, Maxime P.
MARX, Almuth
HOEFLER, Heinz
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SCHMITT, Armin
SCHMITT, Manfred
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Pred. No. 3;
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US-10-449-902-22046
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SEQ ID NO 22046
LENGTH: 2019
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Best Local Similarity
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SEQ ID NO 736
LENGTH: 9353
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK072256
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institute
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: DE 10317955.0 PRIOR FILING DATE: 2003-04-17 PRIOR PPLICATION NUMBER: DE 10300096.8 PRIOR FILING DATE: 2003-01-07 PRIOR APPLICATION NUMBER: DE 10245779.4 PRIOR FILING DATE: 2002-10-01
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CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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Local Similarity 49.1%;
                                        1562 AACGTCATCGAGCAGCCGCTCCGCTTCCCCTCCGACGGCGCGCGAGCGCCAGCGCGTCGCGCGT
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448 TATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGC 494
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                                                                                                                                 Conservative
                                                                                                                                              5.48;
                                                                                                                          Score 30.2; DB Pred. No. 1.8; 0; Mismatches
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Pred. No. 3;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9697
LENGTH: 2127
TYPE: TYPE:
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.3
SEQ ID NO 32119
LENGTH: 1114
TYPE: DNA
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Publication No. US20
GENERAL INFORMATION:
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK107045
DATABASE ENTRY DATE: 2002-08-28
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                                         379 TGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCA 438
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439 GCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 AACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGT
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Pred. No. 1.5;
0; Mismatches
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Pred. No. 1.9;
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APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/31,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
SEQ ID NO 430
LENGTH: 1237
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-430
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Search completed: June 15, 2006, 18:04:16 Job time : 64.413 secs
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US-10-511-937-430/c
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APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
                                                                                                                                                                                                                                                                                                       Query Match 5.3%; Score 30; DB 6; Length 1237; Best Local Similarity 67.7%; Pred. No. 1.6; Matches 42; Conservative 0; Mismatches 20; Indels
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                                                                                               1168 GT 1167
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                                                                                                                                                    86 TT 87
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                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                       Gaps
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                          Database
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
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В
                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 2000000000
N Geneseq_8:*
1: geneseqn198
2: geneseqn200
3: geneseqn200
4: geneseqn200
6: geneseqn200
7: geneseqn200
9: geneseqn201
10: geneseqn21
11: geneseqn2
12: geneseqn2
13: geneseqn2
14: geneseqn2
14: geneseqn2
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177
1 gtcttatcgtgacaggacgc.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                            5244920 seqs, 3486124231 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtcttatcgtgacaggacgc.....gcccgcaacgatctggtaaa 177
                                                                                   geneseqn2002as:*
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geneseqn2003bs:*
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geneseqn2000s:*
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geneseqn2004as:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (without alignments)
6515.052 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 18	c 17	c 16	15	14	13	12	c 11	c 10		- 00	n	c	. en		(Regult No.
30	30	30.2	30.6	30.6	30.6	30.8	30.8	_	30.8			32	41	175.4	177	177	177	Score
16.9	16.9	17.1	17.3								17.5	18.1	23.2	99.1	100.0	100.0	100.0	Query Match
1710	657	1127	78869	10968	1404	29169	3600	3448	1342	1268	2109	921	141	5038	2773	564	560	Query Match Length
11	12	14	14	14	13	10	4.	4.	4.	4	14	w	12	12	9	N	12	BB
ABD14088	ADI45632	AEB67418	AEC75774	AEC75808	ADT47065	AAD64735	ABL18800	ABL27502	ABL27503	ABL18801	ADY37449	AAA02474	ADQ48576	ADQ48539	AAL61306	AAV62487	ADQ48575	ID
Abd14088 Pseudomon	Adi45632 Plant iso	Aeb67418 Rice geno	Aec75774 Polyangiu	Aec75808 P. cellul	Adt47065 Bacterial	Aad64735 Human car	Abl18800 Drosophil	Abl27502 Drosophil	Abl27503 Drosophil	Abli8801 Drosophil	Ady37449 DNA encod	Aaa02474 Human col	Adq48576 Viral vec	Adq48539 Viral vec	Aal61306 p2ZOp2F e	Aav62487 O. pseudo	Adq48575 OpIE2 pro	Description

Novel nucleic acid molecule comprising all or a portion of one or more

WPI; 2004-132944/13.

RP,

Welch PJ,

Harwood

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Madden K,

Frimpong

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Franke KE;

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228. 28. 6666	N N N N N N N N N N N N N N N N N N N	00000000000000000000000000000000000000	30 30 30
16.2 16.2 16.2	16.2 16.2 16.2 16.2	16.8 16.8 16.8 16.8 16.7 16.7	16.9 16.9 16.9 16.9
2085 2088 2091 2091	823 915 1425 1425 1434 1443 1551	1311 1370 1789 3915 13579 13579 100 1798 1593 585	2485 3107 3501 6107 6107 6107 132544
6 2 15	12 8 13 11	113 14 113 113	13 6 6 13
ABD13633 AEE86025 AAX06989 ABK90730	ACH89781 AAS70780 AAS51490 ACA19456 ADS56860 ABD13493 ABD13719	ACL65908 ADF83430 ABL19245 ABL19244 ACL64638 AAAA01209 ADT18768 ADD145695 ABD13766	AEF55630 ADS89385 ADS89483 ABK31430 ABL70389 AAS61341 ADV99887
Abd13633 Pseudomon Aee86025 Human neu Aax06989 Human neu Abk90730 cDNA enco	Ach89781 Human gen Aas70780 DNA encod Aas51490 Pseudomon Aca19456 Prokaryot Ads56860 Bacterial Add56860 Becterial Abd13493 Pseudomon Abd13719 Pseudomon	Ac165908 M. xanthu Adf83430 Bread whe Ab119245 Drosophil Ab119244 Drosophil Ab119244 Drosophil Ac164638 M. xanthu Aaa01209 Human col Adt18768 Plant cDN Adt45695 Bacterial Abd13766 Pseudomon	Aef55630 Human gen Ad889385 Oligonucl Ad889483 Oligonucl Abk31430 Signal tr Abl70389 Chemicall Aas61341 Human gen Adv99887 Nanchangm

ALIGNMENTS

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18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-0398617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                                                       viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; OpIE2 promoter.
                                                              (MADD/)
(FRIM/)
                                                                                                                                                                                 18-JUL-2003; 2003WO-US022437.
                                                                                                                                                                                                    29-JAN-2004.
                                                                                                                                                                                                                      WO2004009768-A2.
                                                                                                                                                                                                                                      Unidentified.
                                                                                                                                                                                                                                                                                            OpIE2 promoter DNA sequence
                                                                                                                                                                                                                                                                                                               09-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                   ADQ48575;
                                                                                                                                                                                                                                                                                                                                                   ADQ48575 standard; DNA; 560
                                                                               (INVI-) INVITROGEN CORP.
(BENN/) BENNETT R P.
(WELC/) WELCH P J.
(HARW/) HARWOOD S.
                                                   BENNETT R P.
WELCH P J.
HARWOOD S.
MADDEN K.
FRIMPONG K.
FRANKE K E.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpiE2 promoter that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                            Orgyia pseudotsugata; polyhedrosis virus.
                                                                                                                                                                                                                                                                                                                               Op 1e2; promoter; shuttle vector; transformation; melanotransferrin; immediate early baculovirus promoter; prokaryotic; transcription; bleomycin/phleomycin-type antibiotic; insect cell; transposon;
                                                                                                                                                                                                                                                                                                                                                                   Orgyia pseudotsugata; multicapsid; nucleopolyhedrosis virus; OpMNPV; Op ie2; promoter; shuttle vector; transformation; melanotransferrin;
                                                                                                                                                                                                                                                                                                                                                                                                                   O. pseudotsugata multicapsid nucleopolyhedrosis virus ie2 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of
                     WPI; 1998-557129/47
                                                      Grigliatti TA,
                                                                                                                        27-MAR-1997;
28-JAN-1998;
                                                                                                                                                                                                               08-OCT-1998.
                                                                                                                                                                                                                                               WO9844141-A2
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19-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV62487;
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                                                                                                                                                                           26-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV62487 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 16; 555pp; English.
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                                                                                        (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                              ion transport peptide hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome and further comprising two or more recombination sites that t substantially recombine with each other, useful as gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 144 A; 156 C; 116 G; 144 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                      97US-0049946P.
98CA-02221819.
                                                                                                                                                                           98WO-CA000282
                                                      Theilmann
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                                                    Pfeifer TA,
                                                      Hegedus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 560;
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This represents a Orgyia pseudotsugata multicapsid nucleopolyhedrosis CC virus (OpMNPV) immediate early 2 (Op ie2) promoter sequence. The CC invention provides a new shuttle vector for transforming insect cells CC that comprises: (1) prokaryotic origin of replication; (ii) insect comprises: (1) prokaryotic origin of replication; (ii) insect comprises: (1) prokaryotic origin of replication; (ii) insect cells cearly baculovirus promoter; (iii) prokaryotic promoter sequence, and (iv) CC selectable marker capable of conferring resistance to a bleomycin/CC phleomycin-type antibiotic under transcriptional control of (ii) and CC (iii), in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologous DNA, CC useful to allow study of gene expression and direct expression of heterologous gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologous CC melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell lines from disparate species, allowing screening of lines for optimum constitutes in insect cells. They enable transformation of insect cell used to optimise heterologous protein expression and facilitate selection of desired transformants. (Updated on 17-OCT-2003 to standardise OS
  Best Loc
Matches
                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression vectors for transforming insect cells from disparate lines useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins.
                                                                                                     Sequence 564 BP; 147
  Local Similarity
mes 177; Conserv
100.0%; Score 177; DB 2; llarity 100.0%; Pred. No. 3.1e-48; Conservative 0; Mismatches 0;
                                                                                                        A; 160 C; 116
                                                                                                        G; 141 T; 0 U; 0 Other;
                                                     Length 564;
     Indels
  0,
  Gaps
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RESULT 3
AAL61306
ID AAL6
XX AAL6
XX AAL6
XX P22-S
XX P22-S
XX Mult
KW Mult
KW Uumc
XX Unid
XX Unid
XX Unid
XX Unid
XX 15-N
XX 16-N
XX 16-N
XX 16-N
XX (PH2
PA (KL)
                                                                                                                                                                                                                            Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease; tumour necrosis factor alpha; gene therapy; arthritis; gene; ds.
                                                                                                                                                                                                                                                                             p2ZOp2F expression vector for insect cells.
                                                                                                                                                                                                                                                                                                            22-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                           AAL61306
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                                                                                                                                                                                                                                                                                                           entry)
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16-NOV-2001; 2001DK-00001702. 16-NOV-2001; 2001US-0331575P.

(PHAR-) PHARMEXA AS (KLYS/) KLYSNER S.

15-NOV-2002; 2002WO-DK000764

22-MAY-2003

Unidentified

WO2003042244-A2

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RESULT 4
ADQ48539
ID 48539
ID 48539
ID 48539
AC ADQ4
AC ADQ4
AC Vira
AC Vira
KW vira
KW repl
KW gene
CS Unid
EN WO20
XX
PP 18-J
PR 18-J
PR 24-N
PR (BEI
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(INVI-)
                                                         18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-0398617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                                                                                  replication-defective gene therapy vector; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to immunogenic analogues of multimeric proteins such as immunogenic variants of interleukin 5 (II.5) and tumour necrosis factor alpha (TNF, TNFalpha) and methods for production of immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in gene therapy. The present sequence is p2ZOp2F expression vector for insect cells. This sequence is used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunogenic analogue composition for treating
                                                                                                                                                                                           29-JAN-2004.
                                                                                                                                                                                                                        WO2004009768-A2
                                                                                                                                                                                                                                                                                                                    viral vector; recombination site; recombinant virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ48539 standard; DNA; 5038
                                                                                                                                                                                                                                                                                                                                                 Viral vector-related plasmid
                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2773 BP; 669
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                                                                                                                                                          18-JUL-2003; 2003WO-US022437
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(VOLD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NIEL/)
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INVITROGEN OF BENNETT R P
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BRATT T.
VOLDBORG B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nielsen FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
 G. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                 CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                  e particle generation; gene expression inhibition;
ds; plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a polymeric protein, useful for preparing inflammatory diseases e.g. arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bratt T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 177; DB 9;
Pred. No. 4.5e-48;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                 piB/V5-His-DEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Voldborg B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a plasmid that was used in the exemplification of the invention.
  18-JUL-2002;
26-JUL-2002;
                                                                                                                                                                                                                                                                                        replication-defective particle generation; gene expression gene therapy vector; ds; plasmid; recombination region.
                                                                                                                                                                                                                                                                                                                                             viral vector; recombination site; recombinant virus;
                                                                                                                                                                                                                                                                                                                                                                                               Viral vector-related plasmid pIB/V5-His-DEST recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-2004
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                                                                             18-JUL-2003; 2003WO-US022437
                                                                                                                                                                                       WO2004009768-A2
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(MADD/)
(FRIM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-132944/13
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MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAGGCGCCCGTCCCGCTTATCGCGCCCTATAAATACAGCCCGCAACGATCTGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCACGTGACCGGACA
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2002US-0396335P
2002US-0398617P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                μх
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           555pp; English.
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Pred. No. 1.8e-47;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Madden
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 U;
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RESULT 6
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ID AAA024
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a recombination region of a plasmid that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                               detection; cancerous state; metastasis; identificat oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung can
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colon cancer cell line polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more do not substantially recombine with each other,
                   14-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA02474 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HELC/)
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24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                                                  13-MAY-1999;
                                                                                                                                                       18-NOV-1999
                                                                                                                                                                                                             WO9958675-A2
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA02474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 141 BP; 43 A; 36 C; 27 G; 34 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 17; 555pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FRAN/)
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WELCH P J.
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MADDEN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVITROGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                98US-0085426P
98US-0085537P
                                                                                                  99WO-US010602
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Р.
                                                                                                                                                                                                                                                                                                                                                                  tumour; diagnosis; gene expression
state; metastasis; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.0017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  portion of one or more recombination sites that useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                        product;
breast ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO:2465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                          cancer;
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RESULT 7
ADY37449/c
ID ADY374.
XX ADY374.
XX ADY374.
XX I9-MAY
DT 19-MAY
XX DNA en
XX DNA en
XX ds; gei
XX ds; gei
XX Arthrol
XX Key
FT CDS
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21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of premetastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-negative breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product that a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                               Arthrobacter ureafaciens; IFO12140.
                                                                                                                                                               19-MAY-2005
                                                                                                                                                                                              ADY37449;
                                                                                                                                                                                                                             ADY37449 standard; DNA; 2109 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 921 BP; 239 A; 214 C; 205 G; 223 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 989; 1097pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide library used
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(HYSE-) HYSEQ 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                              gene;
                                                                                                                            encoding
                                                                                                                                                                                                                                                                                                                                         136 GCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                             37
                                                                                                                                                                                                                                                                                                                                                                           97
                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 GACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG
                                                                                                                                                                                                                                                                                                                                                                                                       76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       CGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAGCTGCGCNCCAGGTGGCTGTCCCACGCCGGTCTCCGCGCCTGCCCGGTGCGCGGGT
                                                                                                                                                                                                                                                                                                             TAAGATCGNGCC
                                                                                                                                                                                                                                                                                                                                                                         GGCGTCNAANCCACCTTCCCTTCGTCTCCTCCGGCTCCGCGTTCAGGGAGCGACTGTCCT
                                                                                              diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                              acyl-CoA oxidase
                                                                                                                                                              (first entry)
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98US-0105234P.
98US-0105877P.
                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.1%;
                  .2109
                                                                                              acyl-CoA oxidase.
                                                                                                                                                                                                                                                                                                           26
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Randazzo F, Kennedy GC, I
Crkvenjakov R, Dickson M,
Garcia V, Jones LW, Stac
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
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on M, Drmanac S, I
Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 921;
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RESULT 8
ABIL18801
ID ABIL1
XX ABIL1
XX ABIL1
XX Dros
XX ZY Z7-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to Arthrobacter ureafaciens (IFO12140) acyl-CoA oxidase (I), which has excellent stability in the presence of thiol reagent at 37 degrees C. Also described are: the acyl-CoA oxidase gene (II) encoding (I); recombinant DNA (III) obtained by introducing (II) into a vector DNA; a transformed host or transduced host (IV) containing (III); and preparation of (I). (I) is useful in clinical diagnosis. The present sequence represents DNA encoding acyl-CoA oxidase. Note: The present sequence is not displayed in the specification but was obtained in electronic format directly from WIPO at
                                                                                                         Drosophila; developmental biology; cell signalling; insecticide
                27-SEP-2001
                                           WO200171042-A2
                                                                     Drosophila melanogaster
                                                                                                pharmaceutical;
                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 7876.
                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                    ABL18801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2109 BP; 401 A; 695 C; 662 G; 351 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; SEQ ID NO 2; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel acyl-CoA oxidase exhibiting high stability in presence of thiol reagent at specific pH and temperature, useful in clinical diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bakke M, Kajiyama N;
                                                                                                                                                                                                                                ABL18801 standard; DNA; 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-214252/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences/03.03.2005/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KIKK ) KIKKOMAN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-AUG-2003; 2003JP-00299607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                        1503
                                                                                                                                                                                                                                                                                                                                                               1443 CCGGGCCAGGACGCCAAAGTTGGCGCCACGGAACTCCTTGGCGTAATCGGCCAGGAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                       CITGGCC 1377
                                                                                                                                                                                                                                                                                                                                                                                         ACAGGACGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                     CGCGACCTGCCGCAGGCCTGTCCGGTGCAAGGCCACGCCGCAGCCTGGTCCACGACGTA
                                                                                                                                                                                                                                                                                                                                 CCCGTCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                     (first entry)
                                                                                                gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Acyl-CoA oxidase"
/partial
/note= "No Stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.5%;
52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
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RESULT 9
ABL27503
ID ABL27503
ID ABL27503
AC ABL2
XX ABL2
XX Dros
XX Dros
XX Dros
XX Dros
XX Phar
XX W020
XX 27-8
XX 27-8
XX 23-W
PR 11-J
XX PF 23-W
PR 11-J
XX WPI;
XX WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL01840-ABL16175) and the encoded proteins (ABL018777) ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
               WPI; 2001-656860/75
                                            Venter JC,
                                                                                                      23-MAR-2000;
11-JUL-2000;
                                                                                                                                                  23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                  27-SEP-2001
                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genomic polynucleotide SEQ ID NO 33982.
                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1268 BP; 295 A; 336 C; 360 G; 277 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic a genes from Drosophila
                                                                                                                                                                                                              WO200171042-A2
                                                                                                                                                                                                                                                                       pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                             ABL27503 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 7876; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59;
                                                                          PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC
                                                                          CORP NY.
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                                          Adams M,
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                                                                                                      2000US-0191637P
2000US-00614150
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 1342
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                                            PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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                                            Myers
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                                            E E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
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RESULT 10
ABL27502/c
ID ABL275
XX ABL275
XX ABL275
XX Drosop
XX WO2001
XX WO2001
XX WO2001
XX Unexter
XX PI Venter
XX Venter
XX Venter
XX New if
PI Venter
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PI Interf
XX Claim
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Best Local S
Matches 59
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                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and interactions.
                                                                                                                                             New isolated nucleic a
                                                                                                                                                                                                                                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                           Venter
                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ
                                                                                                                                                                                                                                                         (PEKE )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                            2001-656860/75.
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2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                NO 33979;
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                                                                                                                                           detection reagent for detecting for elucidating cell signaling a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biology; cell signalling; insecticide
                                                                                             21pp +
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Pred. No. 6.7;
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    drugs.
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Similarity

17.4%; 55.7%;

Score 30.8; D Pred. No. 8.5; 0; Mismatches

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Length 3600; Indels

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Sequence 3600 BP; 946 A; 856 C; 823 G; 975 T; 0 U; 0 Other;

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                                                   capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL31515) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-BBD72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 7873; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes from Drosophila and for elucidating cell signaling and ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
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11-JUL-2000; 2000US-00614150
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Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                              protein (CAP) useful for screening a bioactive agent capable of binding to carcinoma associated (CA) protein and for evaluating the effect of a candidate carcinoma drug. The invention also describes the use of novel compositions for use in screening methods and provides compositions and methods associated with altered expression of TBX21 in cancer. Suitable cancers which can be diagnosed or screened by the invention includes acinar cell carcinoma, fibrosarcoma, Kaposi's sarcoma, breast cancer and hairy cell leukaemia. The present sequence is human carcinoma-associated (CA)
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02-MAR-2001; 2001US-00798586.
08-NOV-2001; 2001US-00052482.
                                                                                                                                                                                                                                                                                                                                                 Sequence 29169 BP; 5725 A; 7553 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  candidate carcinoma drug
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(ENGE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vel recombinant carcinoma-associated protein such as mouse or human X21 protein, useful for screening a bioactive agent capable of binding carcinoma associated protein, and for evaluating the effect of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1607
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ENGELHARD E K.
                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                   Conservative
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61.0%;
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Pred. No. 1
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ADT47065
ADT470765
ADT470765
ADT470765
ADT47077
AC ADT477
AC ADT47
                                                    CC promoter functional in a plant cell, where the promoter is positioned to comprise for expression of a polynucleotide encoding a polypeptide from a comprising the recombinant DNA construct and a method of producing a ctransformed plant having an improved property. The plant is a crop plant cell such as maize or soybean. The method of producing a plant with the crecombinant DNA construct and growing the transformed plant cell recombinant DNA construct and growing the transforming a plant with the crecombinant DNA construct is useful for improving plant, where the coll recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plants with the cingroved plant properties, e.g. improved cold, heat or drought tolerance, content, improved plant with plant growth rate by modification of the cell cycle pathway with plant growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or poston poston use and/or uptake, by modification of carbohydrate, nitrogen or production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHEN/)
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GOLDMAN
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Best Local (
                                                                                                                                                                                                                                                                                                        The invention relates to a purified or recombinant nucleic acid (I) comprising a nucleotide sequence encoding a polypeptide involved in or required for the biosynthesis of ambruticin. The complement of the nucleotide sequence hybridizes to a nucleic acid encoding a domain selected from beta-ketoacylsynthase, acyltransferase, beta-ketoreductase, dehydratase, encylreductase, or acyl carrier protein domains of the sorangium cellulosum (synonym: Polyangium cellulosum) ambruticin gene cluster, or where the complement of the nucleotide sequence hybridizes to a nucleic acid encoding an amino acid sequence selected from (SEQ ID NO. 11-19 (AECT5784-AECT5782). The nucleic acid is useful for producing polyketides, including ambruticins and ambruticin analogs and derivatives. Ambruticins can be used for treating fungal infections. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids encoding polyketide synthases and polyketide modification enzymes involved in or required for the biosynthesis ambruticin, useful for producing polyketides, e.g. ambruticins, fo treating fungal infections.
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04-MAY-2004; 2004US-0568290P.
07-MAR-2005; 2005US-00075185.
                                                                                                                                                                                                                              Sequence 10968 BP; 1231 A; 3980 C; 4394 G;
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                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                    sequence represents P. cellulosum ambruticin ambC gene.
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                 CTGCTCCTGTCGGGTCGCGACGAGCCGGCCGCCCAGGCCGGGCGGCTCGCC---
                                                              CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
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                                                                                                                          Conservative
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53.3%;
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Pred. No. 7.
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Mismatches
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3 CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCGAACTCCTTA 62

Matches Query Match Best Local :

, 88 Similarity

Conservative

17.3%;

Score 30.6; Pred. No. 21;

BG

Mismatches

74; 14;

Indels Length

ω , Gaps

Sequence

78869

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10766 A; 27557 C; 28921 G; 11625 T; 0 U; 0 Other;

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RESULT 15
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AC ABC75
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                                                                                            comprising a nucleotide sequence encoding a polypeptide involved in or required for the biosynthesis of ambruticin. The complement of the nucleotide sequence hybridizes to a nucleic acid encoding a domain selected from beta-ketoacylsynthase, acyltransferase, beta-ketoreductase, dehydratase, encylreductase, or acyl carrier protein domains of the sorangium cellulosum (synonym: Polyangium cellulosum) ambruticin gene cluster, or where the complement of the nucleotide sequence hybridizes to a nucleic acid encoding an amino acid sequence selected from (SEQ ID NO. 11-19 (AEC75784-AEC75792). The nucleic acid is useful for producing polyketides, including ambruticins and ambruticin analogs and derivatives. Ambruticins can be used for treating fungal infections. The present sequence represents Polyangium cellulosum ambruticin biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding polyketide synthases and polyketide modification enzymes involved in or required for the biosynthesis ambruticin, useful for producing polyketides, e.g. ambruticins, for treating fungal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2004; 2004US-0551103P
04-MAY-2004; 2004US-0568290P
07-MAR-2005; 2005US-00075185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AEC75776, AEC75777, AEC75778, AEC75779, AEC75780, AI AEC75782, AEC75783, AEC75784, AEC75785, AEC75786, AEC75787, AEC75789, AEC75790, AEC75791, AEC75792, AEC75801, AEC75802,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a purified or recombinant nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 1; 285pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2005; 2005WO-US007924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6892
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                                                                          cluster.
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n complet	22159	123	22099	63	22042	
Search completed: June 15, 2006, 16:31:52 Job time : 192.921 secs	22159 ACGCGCACGCACCTCGCGCGCTCGCGCTCCGCGCCG 22203	123 AGGCGCCCGTCCCCCTTATCGCGCCCTATAAATACAGCCCGCAACG 167	22099 GAGCACCTGCGGCCCACCCGGACCAGCGGCTGCTCGACGTCGCCGCGGGCCTGGCCACG 22158	63 TCGGAACAGGACGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122	22042 CTGCTCCTGTCGGGTCGCGACGAGCCGGCGCCGCCCCAGGCCGGGCGGCTCGCC 22098	



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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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177
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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BY343718 BY343718
BY339252 BY339252
BY083658 BY083658
CF916169 B0991A12-
BQC200008 Talx1138G
CF913548 B0950D02-
AW319335 unl1f04.y
AA989838 uc79f07-y
CF915946 B0987F04-
CF9174622 B0941F09-
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AQ287217 HS 2266 A
BY342594 BY342594
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9 B0991A12-

8 Talr1138G

8 B0950D02-

5 un11f04.y

9 uc79f07.y

5 B0987F04-

2 B0941F09-
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45	44	43	42		C 40		38	37	36	35	c 34	33			c 30		28	27	26	c 25	24	23	22	c 21	20
31.2	31.2	31.2	31.2	31.2	31.2	31.4	31.4	31.4	31.4	31.4	31.6	31.6	31.6	31.8	31.8	31.8	32	32	32.4	32.6	32.8	32.8	33	33	33
17.6	17.6	17.6	17.6	17.6	17.6	17.7	17.7	17.7	17.7	17.7	17.9	17.9	17.9	18.0	18.0	18.0	18.1	18.1	18.3	18.4	18.5	18.5	18.6	18.6	18.6
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CW028427 104_255_1	CL190317 104 408 1	CW502443 fsbb001f2	CW170205 104 580 1	CK066979 73262rsic	CK071906 69075rsic	CG295117 OG5BB59TC	CJ086368 CJ086368	BB843476 BB843476	CJ079027 CJ079027	BY340052 BY340052	BQ720271 AGENCOURT	CL494562 SAIL 597	DX006812 OG_ABa012	CR859367 Pongo pyg	BX463482 BX463482	CR540072 DKFZp459D	BQ645920 AGENCOURT	BY789720 BY789720	CO973145 BeG60N07D		CE066545 tigr-gss-	CW192940 104_615_1	AK144659 Mus muscu	CW919246 EDCA975TR	CA490927 AGENCOURT

ALIGNMENTS

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE LOCUS DEFINITION RESULT 1 DN873866 FEATURES COMMENT SOURCE ORGANISM JOURNAL source Canis familiaris Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; DN873866 822 bp mRNA line nad29c08.yl Dog eye cornea. Unnormalized (nad) cDNA clone nad29c08 5', mRNA sequence. DN873866 DN873866.1 GI:62843807 Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Email: graeme@helix.nih.gov Plate: 29 row: c column: 08 Seq primer: Universal M13 Reverse. Tel: 301 402 3452 Fax: 301 496 0078 Contact: Wistow G Unpublished (2005) NEIBank analysis of Dog cornea Wistow, G. Canis familiaris (dog) Canis. (bases 1 to 822) /Clone lib="Dog eye cornea. Unnormalized (nad)" /clone lib="Dog eye cornea. Unnormalized (nad)" /note="Organ: Eye; Vector: pCMVSport6; RNA was extracted /rom dog cornea tissue. A directionally cloned cDNA library in the pCMVSPORT6 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript /tissue_type="Cornea" /dev_stage="Adult" /lab_host="EMDH10B" /strain="Beagle" /db_xref="taxon:9615" /clone="nad29c08" /organism="Canis familiaris" /mol_type="mRNA" Location/Qualifiers . .822 linear E nad) Canis EST 21-APR-2005 s familiaris

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RESULT 2
AQ297217
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SOURCE
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Matches
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                                                                                                                                                                                                                                                                                                         Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2266 row: A column: 15
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.

(bases 1 to 507)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ297217 507 bp DNA linear GSS 15-DE(HS_2266_A1_A08_MR CIT Approved Human Genomic Sperm Library D | sapiens genomic clone Plate=2266 Col=15 Row=A, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                      401 Queen Anne Avenue North, Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17),
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGCCGCCAGATAACTGTGCCCCGAACCACCGCCGCCTGCGCCCCTCCCCGCCCCGGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGT 132
                                                                                                                                                                                                                                                                quality sequence stop: 507.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid System, full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). Pirst strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGATCGCGAGCGGCCGCC(T)15-3']. CDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC). Analyzed data available through http://neibank.nei.nih.gov."
                                                                                   /clone_lib="CIT Approved Human Genomic Sperm Library D"
note="organ: sperm; Vector: pBeloBAC11; BAC Clones in
                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                organism="Homo sapiens"
|mol_type="genomic DNA"
                                                                                                                                                     .one="Plate=2266 Col=15 Row=A"
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    19.1%;
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,
    Score 33.8;
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    DB 11;
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Length 507;
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Adams, M.D.
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Electher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkini, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Naltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Nawasawa, Y., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Rawasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlsetedt, C., Wang, Y., Watanabe, Y., Yang, L., Zavolan, M., Zhu, Y., Zimer, A., Carninci, P., Hayatsu, N., Hirozane, Kishikawa, T., Komo, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Ragers, J., Hara, A., Hashizume, M., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Myzzaki, A., Sakai, K., Sasaki, D., Shibata, K., Shiraki, A., Sakai, K., Sasaki, D., Shibata, K., Shiraki, A., Sakai, K., Sasaki, D., Shibata, K., Sandisia, G., Free, Francyrintone, M., Sandrana, annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106
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                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag
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                    Bmail: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Icoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
                                                                                                                                                         Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                              12466851
                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 420, 563-573 (2002)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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Sakai, K.,
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Sakazume, N.,
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0; Mismatches
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whole joints Mus musculus
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;
                                                                                                                                                                                                                          Kanagawa 230-0045, Japan
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RESULT 4
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 402)
1 (bases 1 to 402)
1 (bases 1 to 402)
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nagami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 bp mRNA linear EST 06-DEC-2002
BY077721 RIKEN full-length enriched, adult male liver Mus musculus
CDNA clone K630011C08 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. DIVISION of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pippline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY077721.1 GI:26179135
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Tissues were provided by Institute of Immunology 14-16 Al. Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.0%;
Similarity 51.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCGCCCGTCCCGCTTATCGCGCC 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTAATGTGATCCCCCCCCCCTTTCCTTTCTCCGTAGCCTGACGCGGNAGCAGCCGCTTT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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/clone_lib="RIKEN full-length enriched, whole joints"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="L230041A03"
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Pred. No. 8.6;
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CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA 62

Matches Best Local Query Match

75;

Conservative

0; Mismatches Score 33.6; Pred. No. 8.

70;

Indels

0,

Gaps

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Similarity

19.0%;

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ORIGIN

FEATURES

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source
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Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y., Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-171 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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'dev_stage="adult"
'clone_lib="RIKEN full-length enriched, adult male liver"
                                                                                                                                                                                                                                                                                                mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                                                            sex="male"
                                                                                                                                                                                                          clone="K630011C08"
                                                                                                                                                                                                                                                  db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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                                                                                                               tissue_type="liver"
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PUBMED COMMENT

JOURNAL TITLE

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RESULT 6
BY338426
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AUTHORS
TITLE
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                              39 ACCGCAGCCGGACCCCTTATCGGAACAGGACGCCCCCCATATCAGCCGCGCGTT 98
                                                                                                                                                                                                                                                                                                             99 ATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 TCGGAACAGGACGCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACG 122
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                                                                                                                      348 bp mRNA
BY338426 RIKEN full-length enriched, whole
clone L230014G21 5', mRNA sequence.
BY338426
                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Betsy Read
Department of Biological Sciences
California State University San Marcos
333 S. Twin Oaks Valley Road, San Marcos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Haptophyceae; Isochrysidales; Emiliania.

(bases 1 to 931)

Wahlund, T. W., Zhang, X. and Read, B.A.
Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying Cultures of Emiliania huxleyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CV068875

931 bp mRNA linear EST 24-AUG-2004

f2_new_chopped.fasta.Contig488 Preamplified custom cDNA library in
pcMVpport6.1 (ResGen, Invitrogen Inc.) Emiliania huxleyi cDNA, mRNA
                                          Mus musculus
                                                             Mus musculus (house mouse)
                                                                                                       BY338426.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bread@csusm.edu.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Micropaleontology (2004) In press
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
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/clone_lib="Preamplified custom cDNA library in
pcMVsport6.1 (ResGen, Invitrogen Inc.)"
/note="Emiliania huxleyi grown in Artificial Seawater
(Guillard's F/2 media)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Emiliania huxleyi"
/mol_type="mRNA"
/strain="1516"
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Pred. No. 12
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                                                                                                                                                              linear EST 11-DEC-2002 joints Mus musculus cDNA
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AUTHORS
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                                                               FEATURES
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                                            source
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                                                                                    further details.
                                                                                                                                                                                                    prepare mouse tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                     Please visit our web
                                                           Location/Qualifiers
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RS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojbori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Karochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Munatta, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandran, S., Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shirada, K., Okido, T., Rayalor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, L., Yuan, Z., Zavolan, M., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imoteni, K., Ishii, Y., Itoh, M., Kagawa, J., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome resegsc.riken.jp, URL:http://genome.gsc.riken.jp/Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashiraki,Y. Direct Submission

Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated seguence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequence. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-89 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
                                                                                                                                                                                                                                                            Fleming street 16672 Vari,Greece ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                    Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
organism="Mus musculus"
                                                                                                                                                                                                                (http://genome.gsc.riken.go.jp)
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RESULT 7
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                                                                                                                                                                                                            CE 1 (bases 1 to 353)

RRS Okazaki, Y., Furuno, M., Saito, R., Suzuki, H., Yamanaka, I., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gastincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D. R., Namata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Semple, C.A., Setcu, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teaddale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wall, J., Yung, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, I., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Chara, M., Takawa, T., Pukuda, S., Hata, A., Hashizume, W., Imotani, K., Ishia, Y., Natawa, T., Waka, K., Sasaki, D., Shibata, K., Sataki, D., Shibata, K., Shiraki, T., Waki, K., Kawai, D., Shibata, K., Shiraki, Y., Sato, J., Shibata, K., Sasaki, D., Shibata, K., Sato, J., Sato, J., Shibata, K., Sato, J., Jander, E.S., Analyeis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY337247 RIKEN full-length enriched, whole joints Mus musculus cDNA clone L23006D15 5', mRNA sequence.
BY337247
                                                                                                                                                                                           Nature 420, 563-573
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                               Contact: Yoshihide Hayashizaki
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/tissue_type="whole joints"
/clone_Tib="RIKEN full-length enriched, whole joints"
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51.7%;
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   230-0045, Japan
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AUTHORS
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Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384 format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 354)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully
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Fax: 81-45-503-9216
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                                                                                                                                                               musculus (house mouse)
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/tissue_type="whole joints"
/clone_Tib="RIKEN full-length enriched, whole joints"
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/db_xref="taxon:10090"
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clone G730040E06 5', mRNA
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                            354 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243
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                                                                                                                                                                                                                                                                                                lung RCB-0558
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  Bono, H., Kondo, S.,
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                                                                                                         Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RIA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Tel: 81-45-503-9222
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Division of Experimental Animal Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
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                                              /tissue_type="lung"
/cell_line="RCB-0558 LLC"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                organism="Mus
                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                     clone="G730040E06"
one_lib="RIKEN full-length enriched, lung RCB-0558 LLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Petrosky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yana, J., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yanayatsu, N., Hirozame-Kishikawa, T., Wakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Sasaki, D., Shibata, K., Sasaki, D., Shibata, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Haysahizaki, Y., Shibata, K., Shisaki, S., Shasaki, D., Shibata, K., Shaski, S., Shisaki, S., Shisaki, S., Shaski, S., Shisaki, S., Shaski, S., Shisaki,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 CCTCACCAGCTCGCACTCTCCTCGGGGGCGCACGGCTCGCCGTGCCCCTGCCCACCACGG
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75; Conserv
                                                                                                                                                                    Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaga
                                                                                                                                                                                                                                                                                                                                                                                                                   Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
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1 (bases 1 to 355)
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
                                                                                                       Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
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                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                               Nature 420, 563-573
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Matches
                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 TCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
1 (bases 1 to 360)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schombach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schrimil,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY343718 SIKEN full-length enriched, whole joints Mus musculus cDNA clone L230047A12 5', mRNA sequence.
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Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                      Mus musculus
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                              BY343718.1
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="L230028H13"
/tlssue type="whole joints"
/clone_Tib="RIKEN full-length enriched, whole joints"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:10090"
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51.7%;
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ORIGIN

Query Match Best Local Similarity

18.6%;

Score 33; Pred. No.

Length 360

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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Sultana, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Garninci, P.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Garninci, P.,
Yang, L., Yuan, Z., Savolan, M., Shi, X., Kawai, J., Aizawa, K.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagwa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Lahoratory, Forgener Evoluciation Desearch Grane Evoluciation
Contact: Yoshihide Hayashizaki
Lahoratory, Forgener Evoluciation Desearch Grane Evoluciation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                            further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
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Tel: 81-45-503-9222
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                      /mol_type="mRNA"
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/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                 organism="Mus musculus
                                                                                                           clone="L230047A12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dragani, T.A.,
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JOURNAL TITLE

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ACCESSION
VERSION
KEYWORDS
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Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
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Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gassterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
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Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Vang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Yang, L., Yuan, Z., Savolan, M., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Thashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Larkfest 20, 563-573 (2002)
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, K., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Makamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-CTel: 81-45-503-9222
Fax: 81-45-503-9216
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Okazaki, Y., Furuno, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S. Mikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Garimmond,S., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
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BY083658.1 GI:26203394
EST.
Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res
10 (11), 1757-1771 (2000)
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
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/tissue_type="whole joints"
/clone_Tib="RIKEN full-length enriched, whole
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/mol_type="mRNA"
/db_xref="taxon:10090"
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                                        70;
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ORIGIN

FEATURES

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Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Mumata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carrinci, P., Hayatsu, M., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                         /tissue_type="heart"
/dev stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
heart"
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/strain="C57BL/6J"
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                             4; Length 371;
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231 GACAGAGCGTCCCGCTTCCCTCTCC 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF916169 611 bp mRNA linear EST 05-NOV-B0991A12-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0991A12 IMAGE:30480971 5', mRNA sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H. Construction of long-transcript enriched submicrogram amounts of total RNAs by a v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0991 row: A column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11544199
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF916169.1 GI:38187371
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treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/cated to separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/caloroform and Centricon 100. The cDNAs were digested with Sali and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the
                                                                                                                                                                                                                                                                                                                                                                                                                 Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 1: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                primer [Invitrogen:
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'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain="C57BL/6J"
| db_xref="niaEST:B0991A12-5"
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BQ620008
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21 CAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCT 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)

Contact: Dr. Sylvie Cloutier

Cereal Research Centre, Agriculture and Agri-food Canada

195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse
was cloned from the 5' end (same with forward primer and 3'end).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cloutier,S., Dong,G. and Walsh,A.
Wheat functional genomics - Thatcher Lrl cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Liliops clade; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ620008
621 bp mRNA linear EST 28-JUN-200
TaLr1138G03F TaLr1 Triticum aestivum cDNA clone TaLr1138G03F, mRNA
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Plate: 138 row: G column: 03
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
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                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 621)
                                                                                                                                                                                                                                                                                                                                                                                                primer: M13 Forward
                                                 Conservative
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                                                                                                                      /mol_type="mRNA"
/cultivar="Thatcher Lr1"
                                                                                                                                                                                                                                                                                                   db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                  organism="Triticum aestivum"
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                                                                 18.6%;
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Pred. No. 14;
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Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF913548 624 bp mRNA linear EST 05-NOV-2003
B0950D02-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0950D02 IMAGE:30477061 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, t
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0950 row: D column: 02
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treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The
                                                                                                                                                                                                                                                                                                                                                      Site 2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001) [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Unfertilized Egg'
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (house mouse)
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           seq length: 0
seq length: 2000000000
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/AE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/AE_COMB.seq:*
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US-09-902-540-13101
US-09-9252-991A-12370
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US-09-252-991A-12323
US-09-252-991A-12323
US-09-252-991A-12323
US-09-16-121-22
US-09-107-979-22
US-09-107-979-25
US-09-107-979-5
US-09-107-979-5
US-09-107-979-5
US-09-107-13193
US-09-949-016-13193
                    Sequence 12692, A Sequence 2371, App Sequence 1101, Ap Sequence 12370, A Sequence 12337, A Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 5, Appli Sequence 5, Appli Sequence 1393, A Sequence 1393, A Sequence 1398, Ap Sequence 1398, Ap Sequence 674, App Sequence 674, App Sequence 674, App Sequence 11824, Ap Sequence 11824, A Sequence 11823, A Sequence 11823, A Sequence 19425, A Sequence 19426, A Sequence 194
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15.3	15.3	15.3	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.5	15.5	15.5	15.6	15.6
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
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ALIGNMENTS

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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12692
LENGTH: 1710
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12692
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus x
FILE REFERENCE: 38-10(15849)B
                                                                                                                       Sequence 2371, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                            141 TCGCGCCTATAAATACAGCCCGCAACGATCTGGT 174
                                                                                                                                                                                                                                                                                                                                                        414 CCAMAATAGCCGCTCGATCTCTCGGCGAAGTGACGGGGCACCTGGCGAGCGCATTGCCCC
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Mismatches
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US-09-902-540-1101/c
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TYPE: DNA
; ORGANISM: MYXOCOCCUS Xanthus
US-09-902-540-2371
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CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1101
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
                                                                                                                                                                                            Sequence 12370, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 2371
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AND ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/074,788
PRIOR APPLICATION NUMBER: US/074,788
PRIOR APPLICATION NUMBER: US/0704,190
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CURRENT FILLING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 GCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCA 104
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Similarity 55.2%;
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Pred. No. 7.7;
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Pred. No. 4.6;
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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES REL

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTI

TILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTI

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

INVMBER OF SEQ ID NOS: 33142
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12370
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US-09-252-991A-12097
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12097
LENGTH: 1443
Type: min
                                                                                                                                                                                                                                                  Sequence 12323, Application US/09252991A Patent No. 6551795
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NUMBER OF SEQ ID NOS:
SEQ ID NO 12370
LENGTH: 585
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APPLICANT: Marc J.
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SEQ ID NO 12323
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPE
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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Pred. No. 11;
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Pred. No. 9.4;
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; ORGANISM: Beeudomonas aeruginosa
US-09-252-991A-12237
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US-09-252-991A-12237
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12323
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Patent No. 6121415
GENERAL INFORMATION:
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Best Local
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LENGTH: 2085
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CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION:
FILE REFERENCE: 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: EtbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                   COUNTRY:
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                                                                                                                                            1 DNA Way
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Pred. No. 12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6252051
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                  TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                AFFLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: CODIEY, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P10
SEQUENCE CHARACTERISTICS:
LENGTH: 2091 base pair
                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2091 base pair
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REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION, INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                FILING DATE: 3
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Fi
STATE: California
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IDENTIFICATION METHOD:
OTHER INFORMATION:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                  TELEPHONE:
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                                                                      650/225-2066
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Pred. No. 1;
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                                   Matches
                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Appl
Patent No. 699485
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Best Local Similarity
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/09/107,979

FILING DATE: 30-Jun-1998

CLASSIFICATION:
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NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2091 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                      LENGTH: 2091 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                              NAME/KEY: Human NRG3E
LOCATION: 1-2091
IDENTIFICATION METHOD:
OTHER INFORMATION:
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                                   69;
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EDNESS: Single
 ACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGAC 114
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1-2091
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                                                16.2%;
58.0%;
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                              Score 28.6; D
Pred. No. 12;
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Pred. No. 1:
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                                                               Length 2091;
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RESULT 12
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                   Sequence 5, Application Patent No. 6252051
GENERAL INFORMATION:
APPLICANT: Godows
                                                                                                                                                                                                                                                                                                                     Matches
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/899
FILING DATE: 24-Jul-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: 9108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
 APPLICANT: Godowski, TITLE OF INVENTION: E
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STATE: California
                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1-2502
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                  591 ACGCCCAACCGGATTAGCACTCGCCTGACCACCA-TCACGCGGGCGCCCACTCGCTTCCC
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5. 6121415
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                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94080
                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                          Application US/09126121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NRG3B1 (hNRG3B1) / nucleic acid seq.
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58.0%;
, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
ErbB Receptor-Specific Neuregulin Related
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                                                                                                                                                                                                                                                                                                                                           Score 28.6;
Pred. No. 13;
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

1 DNA Way

Genentech, Inc

TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23

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                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09107979 Patent No. 6994856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-JU1-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COnley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      APPLICANT: Godowski, Paul J., Mark, MITLE OF INVENTION: ErbB Receptor-SpeTITLE OF INVENTION: Ligands and Uses NUMBER OF SEQUENCES: 23
                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Human NRG3B
LOCATION: 1-2502
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                   CITY: South San Francisco
                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                            ADDRESSEE:
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VENTION: ErbB Receptor-Specific Neuregulin Related
VENTION: Ligands and Uses Therefor
                                                                                                                                          USA
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                                                                                                                                                                                                                        Genentech, Inc.
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58.0%;
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Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1239, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                         Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 25048
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LENGTH: 2502 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Human NRG3B1 (hNRG3B1) /nucleic acid seq. LOCATION: 1-2502 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/107,979 FILING DATE: 30-Jun-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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  6380
                                                                                                                                                      6260 TTTTTTTGACGACACTCCACCCATCGATGTTGGTACCAGGGGGTGGAAACATCGAAATCA 6319
                                       124
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                                                                                                                 64 CGGAACAGGACGCCCCCATATCCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 ACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGAC 114
                                                                                                                                                                                                                                     76;
                                                                                                                                                                                             4 TTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTAT 63
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                                   GGCGCCCGTCCCGCTTATCGCGCCTATAAATACAG 158
GCGGCCGTCCCCACCACCTCCAGAGTAAAGACAG 6414
                                                                            CGTTCATGGAGTTCCCCCGGAAGCAGCCTTTGGCAACCTCACATTGGGGATCGTGAGCGT 6379
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58.0%;
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Pred. No. 22;
0; Mismatches
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Pred. No. 13;
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                                                                                                                                                                                                                                                                          Length 25048;
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RESULT 15

US-09-99-016-13983/c

Sequence 13983, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-0-08

PRIOR FILING DATE: 2000-0-09

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-0-09
Search completed: June 15, 2006, 17:18:11 Job time : 62.6721 secs
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FEATURE:
FEATU
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SOFTWARE: FRACSEQ for Windows Version 4.0
SEQ ID NO 13983
LENGTH: 57320
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.0%; Score 28.4; DB 3; Length 57320; Best Local Similarity 49.3%; Pred. No. 31; Matches 74; Conservative 0; Mismatches 76; Indels 0;
                                                                                                                                                                                                                                                             1914 GGCGCGGGGCGACCGGGACAGCGCGCA 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1974 GCGCGTCACTTCCGGGAGCGCGCCCCCGCCCCGCGTCACAGCGGACTCCGCCCCCGGCG 1915
                                                                                                                                                                                                                                                                                                                                                                                     135 CGCTTATCGCGCCTATAAATACAGCCCGCA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 GCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCGTCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 GGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGAC 74
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                    and is
                                                                                                                                                                          175.4
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32.23
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30.83
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1: EMC_Celerra_SIDSJ/ptodata/2/pubpna/US00_PUBCOMB.seq:*

2: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US00_PUBCOMB.seq:*

3: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US00_PUBCOMB.seq:*

4: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US00_PUBCOMB.seq:*

6: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

6: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

9: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

10: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

10: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

11: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

12: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

13: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

14: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

15: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
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Query
Match
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9 US-10-156-761-2538
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13 US-11-097-143-38492
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          Sequence 14, Appl Sequence 126, App Sequence 60, Appl Sequence 60, Appl Sequence 89, Appl Sequence 127, Appl Sequence 127, App Sequence 127, App Sequence 149, App Sequence 2538, Ap Sequence 25442, A Sequence 38495, A Sequence 38491, A
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100.0%; Score 177; DB 3; Length 462; iimilarity 100.0%; Pred. No. 2.9e-54; 100.0%; Pred. No. 2.9e-54; Conservative 0; Mismatches 0; Indels 0; Gaps GICTTATCGTGACAGGACGCAACTCCT GITTATCGTGACAGGACGCAACTCCT GITTATCGTGACAGGACGCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT GITTATCGTGACAGGACGCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT TATCGGAACAGGACGCGCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACTCCT [/09896888A SERPITE SH COLUMBIA EXPRESSION VECTORS US/09/896,888A -06-29 IS/09/048,911 -26 -27 PINCE P	ALIGNMENTS	US-10-215-862-22 US-10-944-116-22	US-09-877-665-22 US-10-136-573A-22	US-10-369-493-32534 US-09-817-647-22	US-09-815-242-4072 US-10-282-122A-7326	US-10-029-386-22976 US-10-450-763-6584	US-09-925-065A-711960 US-10-425-115-65984	US-10-369-493-44133	US-10-437-963-5867	US-10-739-930-4094 US-10-437-963-72869	US-11-097-143-26107 US-10-779-543-7296	US-10-275-311A-10 US-11-097-143-26108	US-10-221-613-303	US-10-437-963-55473 US-10-259-194A-563	US-11-075-185-1 US-10-437-963-42126	11-075-185-		
		th 462; els 0; Gaps 0; GCCGGACGCAACTCCT 60	Promoter		Sequence 22, Appl Sequence 22, Appl	Sequence 22, Appl Sequence 22, Appl	Sequence 32534, A Sequence 22, Appl	Sequence 4072, Ap Sequence 7326, Ap	Sequence 22976, A Sequence 6584, Ap	Sequence 711960, Sequence 65984, A	Sequence 44133, A	Seguence 50761, A	Sequence 4094, Ap	Sequence 26107, Ap Sequence 7296, Ap	11 10	, 10	Sequence 55473, A Sequence 563, App	(0 (1	equence 35,

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                                                                                                                                                                                                                                  Sequence 1, Application US/09896888A
Patent No. US20020116723A1
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
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APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Madden, Knut
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
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SEQ ID NO 126
LENGTH: 560
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Publication No.
                   CURRENT APPLICATION NUMBER: US/09/896,888A CURRENT FILING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: US/09/048,911 PRIOR FILING DATE: 1998-03-26 PRIOR APPLICATION NUMBER: 60/049,946 PRIOR FILING DATE: 1997-03-27 NUMBER OF SEQ ID NOS: 50 NUMBER OF SEQ ID NOS: 50 SOFTWARE: Patentin Ver: 2.0
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PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
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PRIOR TILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/474,940
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
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CURRENT APPLICATION NUMBER: U$/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR FILING DATE: 2003-07-18
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TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
TYPE: DNA
ORGANISM: Unknown
PEATURE:
OTHER INFORMATION: OPIE2 promoter sequence
ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 100.0%; Score 177; DB 9 Local Similarity 100.0%; Pred. No. 3e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
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5. US20040219516A1
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; ORGANISM: Orgyia pseudotsugata
US-09-896-888A-1
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CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
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                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc recomb
TOTATION: (593) ... (598
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TYPE: DNA
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                                                                     NAME/KEY: misc recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: ApaLI
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
                 NAME/KEY: misc recomb
LOCATION: (2128)..(21
                                                                                                                                         OTHER INFORMATION: Clai
                                                                                                                                                                                                                           LOCATION: (625)..(630)
OTHER INFORMATION: Clai site
LOCATION: (2128)..(2133)
OTHER INFORMATION: PStI site
                                                                                                                                                                     NAME/KEY: misc recomb
LOCATION: (629)..(634
                                                                                                                                                                                                                                               NAME/KEY: misc_recomb
LOCATION: (625)..(630)
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LOCATION: (586)..(591
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OTHER INFORMATION: Aval site
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LOCATION: (573)..(578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial sequence
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CURRENT APPLICATION NUMBER: US/10/846,911
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: PCT/DK02/00764
PRIOR FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 60/331,575
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 60
SOPTWARE: PATENTIN VERSION 3.1
SEQ ID NO 60
LENGTH: 2773
TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: APALI site US-10-295-074-60
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APPLICANT: NIELSEN, Finn S
APPLICANT: BRATT, Tomas
APPLICANT: VOLDBORG, Bjorr
APPLICANT: MOURITSEN, Sore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity
Matches 177; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VOLDBORG, Bjorn
APPLICANT: MOURITSEN, Soren
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: 674542-2018
PEATURE:
NAME/KEY: misc_recomb
LOCATION: (586)..(591)
                                                                    LOCATION: (561)...(566)
OTHER INFORMATION: HindIII site
PEATURE:
NAME/KEY: misc recomb
LOCATION: (573)...(578)
OTHER INFORMATION: AVAI site
                                                                                                                                                                                         OTHER INFORMATION: p2ZOp2F expression vector for insect cells FEATURE:
NAME/KEY: misc recomb
LOCATION: (561)..(566)
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LOCATION: (2294)..(2299)
OTHER INFORMATION: AVAI, SmaI,
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LOCATION: (2284)..(2289)
OTHER INFORMATION: AVAI site
                                                                                                                                                                                                                                                                                      FEATURE:
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LOCATION: (2551)..(25
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OTHER INFORMATION: NCOI site
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LOCATION: (2204)..(22
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                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                             Sequence 60, Application US/10939107
Publication No. US20050180947A1
GENERAL INFORMATION:
APPLICANT: Pedersen, Hans Rudolf
APPLICANT: Ebert, Bjarke
APPLICANT: Pedersen, Louise Henriet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT: Pedersen, Louise Henriette
APPLICANT: Rasmussen, Peter Birk
TITLE OF INVENTION: NOVel Application of Vaccination Against TNF-alpha
FILE REFERENCE: 674542-2020
CURRENT APPLICATION NUMBER: US/10/939,107
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: PCT/DK03/00147
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: 60/363,128
PRIOR FILING DATE: 2002-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: AvaI,
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LOCATION: (2284)..(2289)
OTHER INFORMATION: AVAI site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI
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LOCATION: (1156)..(11
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OTHER INFORMATION: ClaI site
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LOCATION: (629)..(634
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI
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OTHER INFORMATION: ApaLI site
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OTHER INFORMATION: Clai
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LOCATION: (625)..(630
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177; Conserv
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100.0%; Pred. No. 3.8e-54;
ative 0; Mismatches 0;
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; PEATURE:
; AAME/KEY: misc_recomb
; LOCATION: (2551)..(2556)
; OTHER INFORMATION: APALI site
US-10-939-107-60
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Best Local Similarity
Matches 177; Conserv
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: AVAI, SmaI,
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LOCATION: (2204)..(2209)
OTHER_INFORMATION: NCOI site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PStI
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LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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LOCATION: (586)..(591)
OTHER_INFORMATION: ECORI site
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LOCATION: (573)..(578)
OTHER INFORMATION: AvaI site
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LOCATION: (561)...(566)
OTHER_INFORMATION: HindIII site
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: AvaI site
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LOCATION: (1156)..(11
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LOCATION: (625)..(630)
OTHER_INFORMATION: ClaI site
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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OTHER INFORMATION: Apall site
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                      121 CGAGGCGCCCGTCCCCGCTTATCGCGCCCTATAAATACAGCCCGCCAACGATCTGGTAAA 177
                                                                                  415 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA
                                                                                                                                                                      355 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                            61 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
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CGAGGCGCCCGTCCCGCCTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
                                                                                                                                                                                                                                                      100.0%; Score 177; DB 10; larity 100.0%; Pred. No. 3.8e-54; Conservative 0; Mismatches 0;
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RESULT 7
US-10-622-088-89
US-10-622-088-89
; Sequence 89, Application US/10622088
; Publication No. US20040219516A1
          APPLICANT: Harwood, Steven
APPLICANT: Madden, Knut
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Rec
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/US03/22437
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; OTHER INFORMATION: pIB/V5-His-DEST
US-10-622-088-89
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                                                                                                                                                                                                                                                                                Sequence 127, Application US/10622088 Publication No. US20040219516A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 89
LENGTH: 5038
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PRIOR FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR FILING DATE: 2002-11-19
PRIOR PPLICATION NUMBER: US 60/456,496
PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/474,940
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CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
                                                                                                                                                                                                                                   APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J.
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APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harwood, Stever APPLICANT: Madden, Knut
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PRIOR FILING DATE: 2003-07-18
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               471
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Pred. No. 1.6e-53;
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                                                                                                                    Recombination
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CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR FILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-324
PRIOR PILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KRY: misc_feature; LOCATION: (141)..(148); OTHER INFORMATION: n may be any nucleotide US-10-622-088-127
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PRIOR FILING DATE: 2002-07-26
PRIOR PELICATION NUMBER: US 60/427,231
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR APPLICATION NUMBER: US 60/474,940
                                                                                                                                                      SEQ ID NO 149
LENGTH: 325
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 149, A Publication No.
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LENGTH: 147
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APPLICANT:
APPLICANT:
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APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 0942.5450007
                                                                             FEATURE:
OTHER INFORMATION: Recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Recombination region of pIB/V5-His-DEST FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
                    NAME/KEY: misc feature LOCATION: (141) ... (142)
OTHER INFORMATION: n is
                                                                                                                               ORGANISM: Artificial
                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/396,335
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Madden, Knut
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5. US20040219516A1
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100.0%; Pre
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Pred. No.
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                                                                                    of pIB/V5 His
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2538
LENGTH: 3138
                                                                                                                                       ; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: HORIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
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US-10-156-761-1
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US-10-156-761-2538/c
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                               APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
PRIOR APPLICATION NUMBER: JP 2001-204089
                CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Streptomyces avermitilis FEATURE:
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LOCATION: (145)..(276)
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LOCATION: (1)
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HORIKAWA, HIROSHI
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Pred. No. 0.00018;
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CURRENT FILING DATE: 2300-2410

CURRENT FILING DATE: 2004-02-12

PRIOR APPLICATION NUMBER: 10/776,555

PRIOR APPLICATION NUMBER: 09/217,471

PRIOR APPLICATION NUMBER: 09/217,471

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1997-12-23

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-04-03

PRIOR PILING DATE: 1998-04-03

PRIOR PILING DATE: 1998-04-03

PRIOR PILING DATE: 1998-10-21

PRIOR APPLICATION NUMBER: 60/105,234

PRIOR APPLICATION NUMBER: 09/297,648

PRIOR PILING DATE: 1998-10-21

PRIOR PILING DATE: 1998-01-28

PRIOR APPLICATION NUMBER: 60/072,910

PRIOR PILING DATE: 1998-01-28

PRIOR PILING DATE: 1998-01-28

PRIOR APPLICATION NUMBER: 60/075,954

PRIOR PILING DATE: 1998-03-31

PRIOR FILING DATE: 1998-03-31

PRIOR PRIOR PILING DATE: 1998-03-31
US-10-779-543-8561
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, LOCATION: (4187715)
, OTHER INFORMATION: a, 1
US-10-156-761-1
                                                                                                                                                                                                                       Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8561
LENGTH: 921
TYPE: DNA
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
RUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENCTH: 9025608
TYPE: DNA
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Best Local Similarity
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  ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4, 6, 29, 88, 91, 146, 218, 378, 413, 482, 485, 500, 508,
LOCATION: 531, 573, 577, 585, 623, 637, 642, 651, 662, 697, 704, 724,
LOCATION: 731, 778, 835, 837, 839, 842, 852, 868, 882, 884, 885, 891,
LOCATION: 892, 899, 901
OTHER INFORMATION: n = A,T,C or G
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milarity 61.2%;
Conservative
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Pred. No. 1
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US-11-097-143-25442
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Publication No. US20050208558A1

GRMERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 25442
LENGTH: 1268
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                                                                                                                                                       Matches
                                                                                                                                                                                         Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PELLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                     Local Similarity
717
                                                                          657 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 GCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 GGCAGCTGCGCNCCAGGTGGCTGTCCCACGCCGGTCTCCGCGCCTGCCCGGTGCGCGGGT
                                    77
                                                                                                            17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 TAAGATCGNGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 GGCGTCNAANCCACCTTCCCTTCGTCTCCCGGCTCCGCGTTCAGGGAGCGACTGTCCT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 CGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
                                                                                                                                                       59;
                                  GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                       Conservative
                                                                                                                                                                     17.4%;
55.7%;
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51.5%; Pred. No. 0.43;
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                                                                                                                                                Score 30.8; DE Pred. No. 1.2; 0; Mismatches
                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEIC ACID
EXPRESSION OF 10,000 OR MORE
                                                                                                                                                                                         DB 13;
                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
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                                                                                                                                                       Indels
                                                                                                                                                                                           Length 1268;
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                                                                            716
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                                                                                                                                                       0
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RESULT 14 US-11-097-143-38495

Sequence 38495, Application US/11097143 Publication No. US20050208558A1 GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

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CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/184,831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: DROSOPHILA US-11-097-143-38495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR PILICATION NUMBER: 60/175,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38494, Application US/11097143 Publication No. US20050208558A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Fast
SEQ ID NO 38495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 43008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                791 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             731 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 ACGCCAGCTTCCCTGTGTTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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55.7%;
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                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-38494
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                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 38494
LENGTH: 3448
                                                                                                                   Matches
                                                                                                                                               Query Match
                                                                                                                                   Local
 1607
                                                         1667 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC
                                                                                    17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                            77 GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                     59;
                                                                                                                                   Similarity
GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 1562
                                                                                                                     Conservative
                                                                                                                                17.4%;
                                                                                                                  Score 30.8; DB Pred. No. 1.5; 0; Mismatches
                                                                                                                   0,
                                                                                                                                                 BB
                                                                                                                     47;
                                                                                                                                                 13;
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                                                                                                                                               Length 3448;
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76

Search completed: June 15, 2006, 18:02:55 Job time: 611.121 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on:
        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                             \begin{smallmatrix} 2 & 2 & 3 & 5 & 6 \\ 0 & 5 & 6 & 6 & 6 \\ 0 & 6 & 6 & 6 & 6 \\ 0 & 6 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 \\ 0 & 6 & 6 
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seq length: 2000000000
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA New:*

1. /BMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*

2. /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*

3. /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4. /BMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

5. /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

6. /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7. /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

8. /EMC_Celerra_SIDS3/ptodata/1/pubpna/US0_NEW_PUB.seq:*
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Gapop 10.0 , Gapext 1.0
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        gtcttatcgtgacaggacgc.....gcccgcaacgatctggtaaa
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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      BB
        US-10-449-902-2563
US-10-449-902-2904
US-10-449-902-2904
US-10-449-902-2969
US-10-449-902-2564
US-10-517-441-491
US-10-517-441-491
US-10-449-902-1668
US-10-449-902-1668
US-10-449-902-125610
US-10-449-902-12192
US-10-449-902-16716
US-10-449-902-16716
US-10-449-902-17916
US-10-449-902-17961
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Sequence 2563, Ap
Sequence 19810, A
Sequence 22046, A
Sequence 36119, Ap
Sequence 31119, App
Sequence 401, App
Sequence 24699, A
Sequence 24699, A
Sequence 14247, A
Sequence 15112, A
Sequence 15116, Ap
Sequence 16716, Ap
Sequence 16716, Ap
Sequence 1751, App
Sequence 1761, A
Sequence 17761, Ap
Sequence 17761, Ap
Sequence 17761, Ap
Sequence 7751, App
Sequence 7751, App
Sequence 1773, App
Sequence 1773, App
Sequence 1773, App
Sequence 1779, App
Sequence 1799, Ap
Sequence 1299, Ap
Sequence 1299, Ap
Sequence 1299, Ap
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B 8	Matches Qy	RESULTUS-10-0 US-10-0 Seq. GENN GENN APP APP APP APP APP APP APP APP APP A		C 443	00				n www		ก
199 G 76 C 139 C	16	SEQUET 1 Sequence 2563, Application US/104- Publication No. US20060123505A1 GENERAL INFORMATION: APPLICANT: National Institute of APPLICANT: Bio-oriented Technol APPLICANT: The Institute of PM/A APPLICANT: The Institute of PM/A APPLICANT: FOUNDATION: FULL-LENGTH FILE REFERENCE: MOA-A0205Y1-US CURRENT APPLICATION NUMBER: US/10 CURRENT APPLICATION NUMBER: US/10 CURRENT APPLICATION NUMBER: JP 2002 PRIOR APPLICATION NUMBER: JP 2002 PRIOR APPLICATION NUMBER: JP 2002 PRIOR FILING DATE: 2002-05-30 PRIOR FILING DATE: 2002-05-30 PRIOR FILING DATE: 2002-12-11 NUMBER OF SEQ ID NOS: 56791 SOFTMARE: PatentIn Ver. 2.1 SEQ ID NO 2563 LENGTH: 1127 TYPE: DNA ORGANISM: Oryza sativa PUBLICATION INFORMATION: DATABASE ENTRY DATE: 2002-08-28 DATABASE ENTRY DATE: 2002-08-28 S-10-449-902-2563		24 24 25 80							
GCCCCCGCTCGCCATCGCCATCGCCATCTCGACCTCGACCTCGCACCAGATCT CGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC	GACGCCAGCTTC	19-902-2563/c 19-902-2563, Application US/10449902 2ation No. US20060123505A1 LINFORMATION: ICANT: National Institute of Agrol ICANT: Hio-oriented Technology R ICANT: The Institute of Physical ICANT: Foundation for Advancement 3 OF INVENTION: FULL-LENGTH PLANT REFERENCE: MOA-A0205Y1-US 2NT APPLICATION NUMBER: US/10/449 2NT FILING DATE: 2003-05-29 2 APPLICATION NUMBER: JP 2002-203: 2 FILING DATE: 2002-05-30 2 APPLICATION NUMBER: JF 2002-203: 3 FILING DATE: 2002-12-11 2R OF SEQ ID NOS: 56791 2R OF SEQ ID NOS: 56791 2R OF SEQ ID NOS: 56791 2NARE: PatentIN Ver. 2:1 2NO 2563 3TH: 1127 3: DNA INTON INFORMATION: BASES ACCESSION NUMBER: AK114298 UBASE ENTRY DATE: 2002-08-28 19-902-2563 Match		14.1 14.1 14.1		N N	444	44		ທ ທ	
TCAGCCGCC	ative TCCTGTGTT	nstitut nstitut tted Tec tute Of n for A NOISEN: UMBER: UMBER: JP 02-05-3 BER: JP 02-05-3 C-05-3 C-05-3 Va ON: UMBER: Va ON:		1924 2619 6 3330 6 937 6	00	5 00 0	თთთ	7 '	1 7 6	თ თ	6 7
ATCGCCGGC	Pred. NO. 0.15 0; Mismatches GCTAACCGCAGCCGG	Sequence 2563/c 10-449-902-2563/c bequence 2563, Application US/10449902 bblication No. US20060123505A1 ENERAL INFORMATION: APPLICANT: National Institute of Agrobiol APPLICANT: Bio-oriented Technology Resea APPLICANT: The Institute of Physical and APPLICANT: Foundation for Advancement of TITLE OF INVENTION: FULL-LENGTH PLANT CDN FILE REFERENCE: MOA-A0205Y1-US CURRENT APPLICATION NUMBER: US/10/449,902 CURRENT FILING DATE: 2002-05-30 PRIOR APPLICATION NUMBER: JP 2002-203269 PRIOR FILING DATE: 2002-05-30 PRIOR APPLICATION NUMBER: JP 2002-383870 PRIOR APPLICATION NUMBER: JP 2002-383870 PRIOR APPLICATION VEY. 2.1 NUMBER OF SEQ ID NOS: 56791 SOFTWARE: PATENTIN VEY. 2.1 LENGTH: 1127 TYPE: DNA ORGANISM: OTYZA SATIVA DATABASE ENTRY DATE: 2002-08-28 LOA449-902-2563 LOA449-902-2563	ALIGNMENTS	US-10-449 US-10-449 US-10-449 US-10-449	US-10-449 US-10-449	US-10-449	US-10-953 US-10-449 US-10-449	US-11-313	US-10-449 US-11-121	US-10-449 US-10-449	US-11-217 US-10-449
GCCGCCCGCGTCGTCCGCCATCGCCGGCGCCCCGACCTCGCACCAGATCT CGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC	SIMILATITY 53.9%; Pred. NO. 0.15; Conservative 0; Mismatches 53; Indels 0; Gaps GACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG	·	ENTS	US-10-449-902-18809 US-10-449-902-12737 US-10-449-902-12737 US-10-449-902-1893	-902-22687 -902-17975	-902-27203 -902-476	-349-31139 -902-12832 -902-12783	-529-681	-902-25676 -154-173	-902-14093 -902-21824	-529-77046 -902-8137
ACCTCGCAC	Indels ACTCCTTATO	iences. icement Inst Cement Inst Conal Scien S THEREOF			•						
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TCCG 14		ä.		18809, A 12737, A 1893, Ap	22687, 17975,	27203, 476. Ap	12832,	581, Ap	25676, 173, Ap	14093, 21824,	77046, B137, A

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.

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CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILLING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
NUMBER OF SEQ ID NOS: 56791
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SEQ ID NO 22046
LENGTH: 2019
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LENGTH: 1128
                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: OTYZB BBLIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK072256
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: OTYZA BATIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK070153
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
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CURRENT FILING DATE: 2003-05-29
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                                                                                               1562 AACGTCATCGAGCAGCCGCTCCGCTTCCCCTCCGACGGCGCCAGCGCCGTCGCGCGT 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 CCCCCCGCTCTCCCCGCACGCGATCCGACGCGGGGCGCTCGGTGACGGTGAGGCC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 GCCGCCCGCGTCCGCCATCGCCGGCGCCCCGACTCGACCTCGCACCAGATCTCTCCG
                              98 TATCTCATGCGCGTGACCGGACACGAGGCGCCCGGTCCCGCTTATCGC 144
                                                                                                                                            38 AACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGT 97
                                                                                                                                                                                               59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 CGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 GACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
GACCTCATCCGCGGCCTGCTCGTCAAGGAGCCCCACAAGCGGATCGC 1668
                                                                                                                                                                                            Conservative
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53.9%;
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                                                                                                                                                                                                                Score 30.2; DB 6;
Pred. No. 0.18;
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                                                                                                                                                                                                                                          Length 2019;
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CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
FRIOR APPLICATION NUMBER: JP 2002-203269
FRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 9697
LENGTH: 2127
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; ORGANISM: Triticum aestivum
US-10-953-349-32119
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                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.3
SEQ ID NO 32119
LENGTH: 1114
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Publication No. US20066107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579FUS2
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Publication No. US20060123505A1
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Best Local Similarity
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: OTYZE SELLYE
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK107045
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1543 AACGTCATCGAGCAGCCGCTCCGCTCCCCTCCGACGGCGCGCCAGCGCCGTCGCGCGT
                                                                                        98 TATCTCATGCGCGTGACCGGACACGAGGCGCCCGCTCCCGCTTATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 AACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGT
                                 89 GCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGC 146
                                                                                                                                      29 TGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
GCCGCATGATTGCGTGTTCTCGTGCCGGGTCTCGACGGGGCCGGCTGGCCTCCCCGCGC 838
                                                                                                                                                                                      Conservative
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Pred. No. 0.17;
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                                                                                                                                                                                 Indels
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                                                                                                                                                                                              US-10-517-441-499/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 401
LENGTH: 3107
TYPE: DNA
ORGANISM: Artificial Sequence
                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                           Sequence 499, A Publication No.
                                                                                                                                                 GENERAL INFORMATION:
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Best Local 9
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                     APPLICANT:
                                                                                                                             APPLICANT: FOEKENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast centrates of INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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      APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                          1959 CACTTCCTCCCAATATCGCGCC 1938
                                                                                                                                                                                                                                                                                                                                                                                       2079 AACGCGAAACCACCCGCTCCTCCTCGCTCTCCAACCGCCGAAATAACCTCAACCGCC 2020
                                                                                                                                                                                                                                                                                                                                                     66 GAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
                                                                                                                                                                                                                                                                                                                                                                                                                   6 ATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                         CGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                       GAACCCGCGACTCTTCCTCATTTTAAACAACTTCCTTAACGCGCCCGAACAAACGACCCG 1960
MARTENS, John
MODEL, Fabian
NIMMRICH, Inko
RUJAN, Tamas
SCHMITT, Armin
                                                             HARBECK, Nadia KOENIG, Thomas MAIER, Sabine MARTENS, John
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SCHMITT, Manfred
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                                                                                                                                , John
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Pred. No. 0.23;
0; Mismatches
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; TYPE: DNA
; ORGANISM: OTYZA BATIVA
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK101091
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-25649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
                                                                                                                                                                                                                    PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25649
LENGTH: 2214
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Query Match
Best Local Similarity
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SEQ ID NO 499
LENGTH: 3501
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 2002-203269
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APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: MARX, Almuth
TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
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les 72; Conserv
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Score 29.6;
Pred. No. 0.
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Pred. No.
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                      Length 2214;
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Best Local S
Matches 65
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LENGTH: 2586
TYPE: DNA
ORGANISM: Oryza sativa
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                                                   APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
CURRENT FILING DATE: 2003-05-29
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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PRIOR FILING DATE: 2002-5-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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DATABASE ACCESSION NUMBER: AK100132
DATABASE ENTRY DATE: 2002-08-28
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                                                                                                                                                                                                                                                                                                                                        186
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52.4%;
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APPLICANT: National Institute of Programmer of Applicant: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLS OF INVENTION: FULL-LENGTH PLANT CNNA AND USES THEREOF
FILE REFERENCE: MOA-0A205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
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Publication No. US20060123505A1
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 16689
LENGTH: 2618
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                        Query Match
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DATABASE ACCESSION NUMBER: AK064860
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: National Institute of Agrobiological Sciences APPLICANT: Bio-oriented Technology Research Advancement APPLICANT: The Institute of Physical and Chemical Resear
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ORGANISM: Oryza fativa
ORGANISM: Oryza fativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK067165
DATABASE ENTRY DATE: 2001-12-06
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PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
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                                                                                                                                                                                                                                              Local
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522 TGAGATATAAAATGGCCCTGAGCGACGATGATGATACC 485
                                                   93
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                                                                                                                                                           33 TTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCG 92
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                                                                                                                                                                                                                                              Similarity
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                                                   CGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 130
                                                                                                          TGGGGATCCACACCGTTAGATAACTTATTCTTCGAACGAGCAGGGCCCCCATTTCAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCAAGAGCGCCGACCGCCGCGGCGCTCGCCGCCGCTCCCCACCGGTTCCCGGCAC
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                                                                                                                                                                                                                                     Score 27.6; DI
Pred. No. 1.1;
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                        DB 6;
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                                                                                                                                                                                                                                                                     Length 788;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12192
LENGTH: 2150
TYPE: DNA
ORGANISM: OYZZA SATIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK109540
DATABASE ENTRY DATE: 2002-08-28
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SEQ ID NO 25610
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Best Local :
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                                                  Query Match
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER: OF SEQ ID NOS: 56791
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REPERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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TYPE: DNA
ORGANISM: Oryza sativa
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK101052
DATABASE ENTRY DATE: 2002-08-28
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
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                          / Match 15.4%;
Local Similarity 53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG 75
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 1.9;
0; Mismatches
     0
                          Score 27.2;
Pred. No. 2
     Mismatches
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                                                  DB 6;
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                                                  Length 2150;
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Gaps
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FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOPTWARE: PACENTIN Ver. 2.1
SEQ ID NO 16716
LENGTH: 1774
TYPE: DNA
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; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16716, Application US/10449902
Publication No. US20060123505A1
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
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NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
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APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTCACAAAATTGCTGCTATTAGTGCTGCCAACGGGGTCAAAAAGCTAGTTATTGGCCA 269
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KODAMA, YUKIKO
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Pred. No. 2.6;
0; Mismatches
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